OM protein - protein search,   GenCore version 5.1.6
Run on: November 16, 2005, 21:32:27 ; Search time 165 Seconds
                                                   (without alignments)
                                                   548.497 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSQSSHA.........EAGSEAEEKQDSEKPLLEL 234
Scoring table: BLOSUM62
Searched: 2105692 seqs, 38760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
Database :   A_Geneseq_16Dec04:*
                  1: geneseqp1980s:*
                  2: geneseqp1990s:*
                  3: geneseqp2000s:*
                  4: geneseqp2001s:*
                  5: geneseqp2002s:*
                  6: geneseqp2003as:*
                  7: geneseqp2003bs:*
                  8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES

No.   Score   Match Length DB ID   Description
RESULT 1
ID AAU29056 standard; protein; 234 AA.
DE Human PRO polypeptide sequence #33.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 4; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 2
ID AAM39929 standard; protein; 234 AA.
DE Human polypeptide SEQ ID NO 3074.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   100.0%; Score 1195; DB 4; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 3
ID AAB87532 standard; protein; 234 AA.
DE Human PRO1864.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 4; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 4
ID ABG95857 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 5; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 5
ID ABB84847 standard; protein; 234 AA.
DE Human PRO1864 protein sequence SEQ ID NO:62.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 5; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 6
ID ABB95453 standard; protein; 234 AA.
DE Human angiogenesis related protein PRO1864 SEQ ID NO: 62.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
    Query Match   100.0%; Score 1195; DB 5; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 7
ID ABU58432 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027272-A1.
PD 06-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 8
ID ABU87980 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032127-A1.
PD 13-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 9
ID ABU84295 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003033112-A1.
PD 13-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 10
ID ABR66169 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027278-A1.
PD 06-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 11
ID ABR65559 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036159-A1.
PD 20-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 12
ID ABU99499 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040070-A1.
PD 27-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 13
ID ABU82738 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032113-A1.
PD 13-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 14
ID ABU89859 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.

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PN   US20030036147-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 15
ID   ABR68108 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030027264-A1.
PD   06-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 16
ID   ABU96161 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036144-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 17
ID   ABU92592 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036149-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 18
ID   ABO08669 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030044923-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 19
ID   ABO02721 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030044062-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 20
ID   ABR74875 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040056-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 21
ID   ABR94637 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030044926-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 22
PA   (GETH ) GENENTECH INC.
ID   ABU85610 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030036140-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 23
ID   ABU98770 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030013153-A1.
PD   16-JAN-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 24
ID   ABU97985 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030017544-A1.
PD   23-JAN-2003.

     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 25
ID   ABU91691 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030027277-A1.
PD   06-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 26
ID   ABU89384 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030036141-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 27
ID   ABU86225 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036146-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 28
ID   ABU67438 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030036162-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 29
ID   ABU80466 standard; protein; 234 AA.
DE   Human PRO protein #33.
PN   US20030036137-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 30
ID   ABU90882 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030018173-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 31
ID   ABO33941 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO1864.
PN   US20030009013-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 32
ID   ABR99384 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040063-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 33
ID   ABR98774 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040064-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 34
ID   ABO16297 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
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PN   US2003027267-A1.
PD   06-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 35
ID   ABR92197 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036160-A1.
PD   20-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 36
ID   ABO18838 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044925-A1.
PD   06-MAR-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 37
ID   ABR78259 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054474-A1.
PD   20-MAR-2003.
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 38
ID   ABR39937 standard; protein; 234 AA.
DE   Human prostate selective polypeptide Pr340.
PN   WO2003014298-A2.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 39
ID   ABU71958 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003018183-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 40
ID   ABU84995 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032114-A1.
PD   13-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 41
ID   ABO00134 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032101-A1.
PD   13-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 42
ID   ABO11466 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036124-A1.
PD   20-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 43
ID   ABO02111 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040054-A1.
PD   27-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 44
ID   ABU88685 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.

PN   US2003036133-A1.
PD   20-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 45
ID   ABU83380 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036134-A1.
PD   20-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 46
ID   ABO06181 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003022294-A1.
PD   30-JAN-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 47
ID   ABR59217 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027275-A1.
PD   06-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 48
ID   ABO09279 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003027324-A1.
PD   06-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 49
ID   ABO19143 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036118-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 50
ID   ABO11161 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036123-A1.
PD   20-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 51
ID   ABR6779 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036148-A1.
PD   20-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 52
ID   ABO15992 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040060-A1.
PD   27-FEB-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 53
ID   ABO13698 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044916-A1.
PD   06-MAR-2003.
     Query Match   100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 54
ID   ABU71512 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864.
PN   US2003011855-A1.
PD   16-JAN-2003.

PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 55
ID   ABU65601 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein, SEQ ID 66.
PN   US2003036156-A1.
PD   20-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 56
ID   ABO07449 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032117-A1.
PD   13-FEB-2003.
RESULT 57
ID   ABO03636 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036128-A1.
PD   20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 58
ID   ABR67084 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027266-A1.
PD   06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 59
ID   ABO15687 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054483-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 60
ID   ABU55968 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein, PRO1864.
PN   US2003022298-A1.
PD   30-JAN-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 61
ID   ABU72293 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2002182638-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 62
ID   ABU65296 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032102-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 63
ID   ABU95241 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036117-A1.
PD   20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 64
ID   ABU71144 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US2003036143-A1.
PD   20-FEB-2003.

Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 65
ID   ABO07754 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032130-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 66
ID   ABR69995 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032138-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 67
ID   ABR69328 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036132-A1.
PD   20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 68
ID   ABO01469 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003008353-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 69
ID   ABU81271 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003017542-A1.
PD   23-JAN-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 70
ID   ABR60068 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032137-A1.
PD   13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 71
ID   ABR58287 standard; protein; 234 AA.
DE   BCU0092 protein #SEQ ID 20.
PN   WO2003029421-A2.
PD   10-APR-2003.
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 72
ID   ABU90966 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003018168-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 73
ID   ABR67803 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027269-A1.
PD   06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 74
ID   ABR65191 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027268-A1.

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PD   06-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 75
ID   ABR68413 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027274-A1.
PD   06-FEB-2003.
RESULT 76
ID   ABR71825 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032135-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 77
ID   ABU85305 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003022295-A1.
PD   30-JAN-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 78
ID   ABU88995 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003022297-A1.
PD   30-JAN-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 79
ID   ABU83075 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032105-A1.
PD   13-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 80
ID   ABU94931 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032123-A1.
PD   13-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 81
ID   ABU90479 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032108-A1.
PD   13-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 82
ID   ABU83990 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032111-A1.
PD   13-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 83
ID   ABU93641 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032119-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 84
ID   ABR64486 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027263-A1.
PD   06-FEB-2003.

  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 85
ID   ABO27287 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO1864.
PN   US2003009012-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 86
ID   ABR68718 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027271-A1.
PD   06-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 87
ID   ABO06534 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036125-A1.
PD   20-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 88
ID   ABR99079 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040068-A1.
PD   27-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 89
ID   ABU56963 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003027280-A1.
PD   06-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 90
ID   ABU85915 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003022300-A1.
PD   30-JAN-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 91
ID   ABU82202 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036136-A1.
PD   20-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 92
ID   ABU87213 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036138-A1.
PD   20-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 93
ID   ABU83685 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032109-A1.
PD   13-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 94
ID   ABO08059 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003040066-A1.
PD   27-FEB-2003.
  Query Match            100.0%;   Score 1195; DB 6; Length 234;
  Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
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RESULT 95
ID   ABU92482 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO1864.
PN   US2003045684-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 96
ID   ABU81770 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032104-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 97
ID   ABU65934 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036157-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 98
ID   ABU81152 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864.
PN   US2003027212-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 99
ID   ABR59763 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032120-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 100
ID   ABU93951 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036155-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 101
ID   ABU99804 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003022296-A1.
PD   30-JAN-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 102
ID   ABR66474 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027281-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 103
ID   ABR90892 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040058-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 104
ID   ABO53267 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003027986-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 105
ID   ABU94319 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003017540-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 106
ID   ABU79201 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032106-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 107
ID   ABU86530 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032129-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 108
ID   ABU86835 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032131-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 109
ID   ABU94624 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032103-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 110
ID   ABO04551 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032107-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 111
ID   ABR70300 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032139-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 112
ID   ABU98465 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003022301-A1.
PD   30-JAN-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 113
ID   ABR65864 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 114
ID   ABR64581 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027262-A1.
PD   06-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;

RESULT 115
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
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ID   ABU79506 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032110-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 116
ID   ABU92897 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036142-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 117
ID   ABU95856 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036145-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 118
ID   ABU91076 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036154-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 119
ID   ABU90169 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036153-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 120
ID   ABU09584 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044931-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 121
ID   ABO10856 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036150-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 122
ID   ABR70910 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040069-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 123
ID   ABU98269 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 124
ID   ABU87518 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003022293-A1.
PD   30-JAN-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 125
ID   ABU91386 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003032128-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 126
ID   ABU89274 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 127
ID   ABU84600 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032116-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 128
ID   ABR69690 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032122-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 129
ID   ABU80067 standard; protein; 234 AA.
DE   Human PRO protein #33.
PN   US2003036139-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 130
ID   ABU82481 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2002183494-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 131
ID   ABU93336 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003017541-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 132
ID   ABO09889 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003017543-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 133
ID   ABO08974 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036152-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 134
ID   ABU96445 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003027993-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 135
ID   ABU10542 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein #33.
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PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 136
ID ABU72115 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 137
ID ABU95551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032115-A1.
PD 13-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 138
ID ABU96760 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032140-A1.
PD 13-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 139
ID ABR70605 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 140
ID ABO04956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 141
ID ABO08364 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044922-A1.
PD 06-MAR-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 142
ID ABO05571 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032118-A1.
PD 13-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 143
ID ABR73960 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036135-A1.
PD 20-FEB-2003.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 144
ID ABR95552 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
, RESULT 145

ID ABR80849 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 146
ID ABR81154 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 147
ID ABM00850 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 148
ID ABR88452 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 149
ID ABM77273 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 150
ID ABO28757 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 151
ID ABO31502 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 152
ID ABM07919 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003066752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 153
ID ABO40399 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003066682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 154
ID ABO35824 standard; protein; 234 AA.

DE   Human PRO polypeptide #33.
PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 155
ID   ABO43963 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 156
ID   ADA77818 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 157
ID   ABM24758 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104539-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 158
ID   ABO03026 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036131-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 159
ID   ABR90282 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040075-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 160
ID   ABM17196 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 161
ID   ABR94942 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044930-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 162
ID   ABR95247 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044071-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 163
ID   ADB17071 standard; protein; 234 AA.
DE   Human transmembrane PRO polypeptide (SeqID 14).
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 1195; DB 6;   Length 234;
       Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 164
ID   ABO21485 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 165
ID   ABR97749 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 166
ID   ABR87537 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 167
ID   ABM77578 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 168
ID   ABM27808 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064440-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 169
ID   ABM06089 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 170
ID   ABM03595 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 171
ID   ABM35046 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 172
ID   ABM26283 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
       Best Local Similarity 100.0%;   Score 1195; DB 6;   Length 234;
       Query Match   100.0%;   Pred. No. 1.3e-131;
RESULT 173

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ID   ABO48065 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 174
ID   ABR92807 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 175
ID   ABO24568 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 176
ID   ABM11579 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 177
ID   ABM02680 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 178
ID   ABM15976 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 179
ID   ABO27537 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 180
ID   ABM29028 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 181
ID   ABM07004 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068699-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 182
ID   ABM21098 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 183
ID   ABM09444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 184
ID   ABO41314 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 185
ID   ABO36129 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 186
ID   ABO43658 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 187
ID   ABM76358 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003082717-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 188
ID   ABM76054 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104548-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 189
ID   ABM25673 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104542-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 190
ID   ABM25978 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104543-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 191
ID   ABO03331 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036127-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
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    Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 192
ID   ABO02416 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO).
PN   US2003040061-A1.
PD   27-FEB-2003.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 193
ID   ABO44245 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO 1864.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Best Local Similarity  100.0%;   Score 1195; DB 6;   Length 234;
RESULT 194
ID   ABR90587 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036130-A1.
PD   20-FEB-2003.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 195
ID   ABR73655 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Best Local Similarity  100.0%;   Score 1195; DB 6;   Length 234;
RESULT 196
ID   ABO16907 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 197
ID   ABR94332 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044917-A1.
PD   06-MAR-2003.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 198
ID   ABR75839 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044929-A1.
PD   06-MAR-2003.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 199
ID   ABR71215 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059880-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 200
ID   ABR93112 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064465-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Best Local Similarity  100.0%;   Score 1195; DB 6;   Length 234;
RESULT 201
ID   ABR93417 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054478-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 202
ID   ABR87842 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068718-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 203
ID   ABO27842 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064454-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 204
ID   ABO29977 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064461-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 205
ID   ABO33186 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068724-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 206
ID   ABM04874 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068727-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 207
ID   ABM08834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068772-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 208
ID   ABO35434 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068714-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 209
ID   ABO35519 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068758-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195; DB 6;   Length 234;
     Best Local Similarity  100.0%;   Pred. No. 1.3e-131;
RESULT 210
ID   ABO39484 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068776-A1.
PD   10-APR-2003.
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PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 211
ID   ABM10359 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003069407-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 212
ID   ABM11884 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104555-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 213
ID   ABO52030 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049768-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 214
ID   ABO52335 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049771-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 215
ID   ADA19876 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 216
ID   ABO23653 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032134-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 217
ID   ADD17259 standard; protein; 234 AA.
DE   Human transmembrane PRO polypeptide (SeqID 14).
PN   US2003050465-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 218
ID   ABR97139 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 219
ID   ABR86927 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049778-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;

Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 220
ID   ABM10969 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 221
ID   ABM28113 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 222
ID   ABO31112 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 223
ID   ABM15239 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 224
ID   ABM06394 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 225
ID   ABM04205 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 226
ID   ABM22318 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 227
ID   ABM07614 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 228
ID   ABO40704 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.3e-131;

RESULT 229
ID   ABM35351 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 230
ID   ABM33114 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003087374-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 231
ID   ABO52640 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 232
ID   ABO50200 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 233
ID   ABU99194 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040055-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 234
ID   ABO04246 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036164-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 235
ID   ABO05876 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040074-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 236
ID   ABM18416 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 237
ID   ABR97444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 238
ID   ABR80544 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049740-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 239
ID   ABM01155 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 240
ID   ABR88757 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073169-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 241
ID   ABM13409 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064457-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 242
ID   ABM20793 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068711-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 243
ID   ABO41924 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049745-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 244
ID   ABO42534 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 245
ID   ABM10054 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068773-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 246
ID   ABO38569 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 247
ID   ABM32809 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;

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        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 248
ID   ABM22623 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003087373-A1.
PD   08-MAY-2003.
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 249
ID   ABM74834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003096353-A1.
PD   22-MAY-2003.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 250
ID   ADA79610 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003073173-A1.
PD   17-APR-2003.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 251
ID   ABM96224 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054458-A1.
PD   20-MAR-2003.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 252
ID   ABM02375 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059886-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 253
ID   ABR86317 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049758-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 254
ID   ABR86622 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049772-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 255
ID   ABM16586 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 256
ID   ABM29638 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 257
ID   ABO29062 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003066693-A1.

PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 258
ID   ABM23843 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 259
ID   ABM23233 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068753-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 260
ID   ABM22013 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068742-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 261
ID   ABO37654 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068756-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 262
ID   ABM28418 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003082715-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 263
ID   ABM28723 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003082716-A1.
PD   01-MAY-2003.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 264
ID   ABM66367 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068737-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 265
ID   ABM75749 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104547-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
                            100.0%;      Pred. No. 1.3e-131;
RESULT 266
ID   ABM34029 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003096359-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
        Query Match
        Best Local Similarity 100.0%;    Score 1195;  DB 6;   Length 234;
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 267
ID ABM34334 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 268
ID ABO20265 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 269
ID ABO21180 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 270
ID ABO22095 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 271
ID ADA20048 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 272
ID ABO34173 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 273
ID ABR96529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 274
ID ABR85707 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 275
ID ABR99689 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 276
ID ABM00545 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 277
ID ABM00240 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 278
ID ABO29672 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 279
ID ABM23538 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 280
ID ABM29333 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 281
ID ABO38264 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068667-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 282
ID ABO45564 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 283
ID ABM20488 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 284
ID ADA81337 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 285
ID ABO16602 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027276-A1.
PD 06-FEB-2003.

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          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 286
ID  ABO18228 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003044920-A1.
PD  06-MAR-2003.
RESULT 287
ID  ABO22655 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003027265-A1.
PD  06-FEB-2003.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 288
ID  ABO22960 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003054461-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 289
ID  ABR92502 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064446-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 290
ID  ABR81459 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003049744-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 291
ID  ABM77883 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003049783-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 292
ID  ABR89672 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003073171-A1.
PD  17-APR-2003.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 293
ID  ABM26588 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003032121-A1.
PD  13-FEB-2003.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 294
ID  ABM13714 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064458-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 295
ID  ABO28452 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.

PN  US2003064460-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 296
ID  ABO30282 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003064464-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 297
ID  ABM07309 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068702-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 298
ID  ABM03900 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068734-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 299
ID  ABO37044 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068719-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 300
ID  ABO41619 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068729-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 301
ID  ABO35214 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003068738-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 302
ID  ABM25063 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003104540-A1.
PD  05-JUN-2003.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 303
ID  ABO47455 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003049742-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
          Query Match          100.0%;   Score 1195; DB 6;   Length 234;
          Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 304
ID  ABO47760 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003049747-A1.
PD  13-MAR-2003.
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PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 305
ID   ABO48370 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049750-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 306
ID   ABO51420 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049766-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 307
ID   ABO51725 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049767-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 308
ID   ABO50505 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049779-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 309
ID   ABR79629 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040078-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 310
ID   ABM16891 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044918-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 311
ID   ABO17923 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032132-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 312
ID   ABO20875 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054462-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 313
ID   ABR96834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054462-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 314
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ID   ABM12189 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064445-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 315
ID   ABM16281 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064449-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 316
ID   ABM24148 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064441-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 317
ID   ABM14629 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068696-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 318
ID   ABM04510 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068712-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 319
ID   ABM06699 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068730-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 320
ID   ABM09139 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073174-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 321
ID   ABO33179 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068775-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 322
ID   ABM75444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104545-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;    Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;    Pred. No. 1.3e-131;
RESULT 323
ID   ABM25368 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104541-A1.
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PD   05-JUN-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 324
ID   ABM19878 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104554-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 325
ID   ABO46784 standard; protein; 234 AA.
DB   Human PRO polypeptide #33.
PN   US2003049762-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 326
ID   ABO47089 standard; protein; 234 AA.
DB   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049765-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 327
ID   ADA83135 standard; protein; 234 AA.
DB   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049752-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 328
ID   ABR71520 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032133-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 329
ID   ABR72130 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032136-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 330
ID   ABR98469 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036129-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 331
ID   ABO06839 standard; protein; 234 AA.
DB   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040053-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 332
ID   ABR84792 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040057-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 333
ID   ABR73350 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN   US2003054467-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 334
ID   ABR76444 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044932-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 335
ID   ABR73045 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027270-A1.
PD   06-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 336
ID   ABM18111 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054469-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 337
ID   ABO20570 standard; protein; 234 AA.
DB   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032126-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 338
ID   ABO25313 standard; protein; 234 AA.
DB   Human PRO polypeptide #33.
PN   US2003054463-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 339
ID   ABO25618 standard; protein; 234 AA.
DB   Human PRO polypeptide #33.
PN   US2003054466-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 340
ID   ABR94027 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059879-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 341
ID   ABR79934 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044738-A1.
PD   13-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 342
ID   ABM11274 standard; protein; 234 AA.
DB   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064469-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
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RESULT 343
ID ABO32881 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 344
ID ABO30587 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 345
ID ABO30892 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 346
ID ABM27198 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 347
ID ABM29943 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 348
ID ABM05479 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 349
ID ABM15544 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 350
ID ABM08529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 351
ID ABO42229 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 352
ID ABO37959 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 353
ID ABO45869 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 354
ID ABM66672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 355
ID ADB20178 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 356
ID ABM19573 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 357
ID ABO49285 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049974-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 358
ID ABO49590 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 359
ID ADA78430 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 360
ID ABR88147 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 6; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 361
ID ADA00345 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864

PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 362
ID ABM26893 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 363
ID ABM03290 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 364
ID ABO39789 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 365
ID ABO49895 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 366
ID ABO50810 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 367
ID ABO05266 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 368
ID ABR74570 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 369
ID ABR77049 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 370
ID ABM17806 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 371
ID ABR95857 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 372
ID ABO21790 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 373
ID ABO19960 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 374
ID ABO24263 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 375
ID ABR86012 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 376
ID ABM10664 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 377
ID ABM76663 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 378
ID ABR89367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 379
ID ABM12494 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 380
ID ABM05784 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068717-A1.

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PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 381
ID   ABO34909 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068728-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 382
ID   ABM02985 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 383
ID   ABM18963 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 384
ID   ABM19268 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 385
ID   ABO46479 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 386
ID   ABO48980 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049757-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 387
ID   ABR69023 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027273-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 388
ID   ABR89062 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036119-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 389
ID   ABR72435 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036120-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;

RESULT 390
ID   ABR74265 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 391
ID   ABO18533 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044921-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 392
ID   ABR80239 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 393
ID   ABM01460 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 394
ID   ABM02070 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 395
ID   ABR87232 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068887-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 396
ID   ABM12799 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 397
ID   ABM30553 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 398
ID   ABM24453 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;  Score 1195;  DB 7;   Length 234;
     Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 399
ID   ABO29367 standard; protein; 234 AA.
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DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068697-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 400
ID  ABO31197 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068710-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 401
ID  ABM14324 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068686-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 402
ID  ABM09749 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003073178-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 403
ID  ABO38874 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068774-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 404
ID  ABM34639 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003104538-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 405
ID  ABO51115 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003049781-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 406
ID  ABO03941 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003036158-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 407
ID  ABO10411 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003036151-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 408
ID  ABR77654 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003040067-A1.
PD  27-FEB-2003.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;

    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 409
ID  ABR78864 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003054456-A1.
PD  20-MAR-2003.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 410
ID  ABO23958 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003054482-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 411
ID  ABR93722 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003054457-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 412
ID  ABM01765 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003059883-A1.
PD  27-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 413
ID  ABM78188 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003049764-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 414
ID  ABR89977 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003073177-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 415
ID  ABM27503 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064442-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 416
ID  ABM13104 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064450-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 417
ID  ABO31807 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068731-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;   Score 1195;  DB 7;   Length 234;
    Best Local Similarity 100.0%;   Pred. No. 1.3e-131;
RESULT 418
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ID   ABM14019 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068683-A1.
PD   10-APR-2003.
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 419
ID   ABM08224 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068754-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 420
ID   ABO40094 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068681-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 421
ID   ABM74529 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003096351-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 422
ID   ABM33724 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003096358-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 423
ID   ABM20183 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104556-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 424
ID   ABO48675 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049756-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 425
ID   ABR72740 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036122-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 426
ID   ABO15382 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036121-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 427
ID   ABR85097 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040065-A1.
PD   27-FEB-2003.

     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 428
ID   ABO15077 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044919-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 429
ID   ABO17212 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040077-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 430
ID   ABM17501 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044928-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 431
ID   ABR85402 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049746-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 432
ID   ABM76968 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054464-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 433
ID   ABO28147 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064459-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 434
ID   ABM22928 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068757-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 435
ID   ABM30248 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068723-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 436
ID   ABM21708 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068741-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 437
ID   ABM21403 standard; protein; 234 AA.
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DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003068744-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 438
ID    ABM14934 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003068766-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 439
ID    ABO41009 standard; protein; 234 AA.
DE    Human secreted/transmembrane protein (PRO) #33.
PN    US2003068694-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 440
ID    ABO36739 standard; protein; 234 AA.
DE    Human secreted/transmembrane protein (PRO) #33.
PN    US2003068715-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 441
ID    ABO37349 standard; protein; 234 AA.
DE    Human secreted/transmembrane protein (PRO) #33.
PN    US2003068726-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 442
ID    ABM75139 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003104544-A1.
PD    05-JUN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 443
ID    ABM33419 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003096357-A1.
PD    22-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 444
ID    ABO46174 standard; protein; 234 AA.
DE    Human PRO polypeptide #33.
PN    US2003049760-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 445
ID    ADA82501 standard; protein; 234 AA.
DE    Human secreted/transmembrane protein (PRO) #33.
PN    US2003049755-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 446
ID    ADB85587 standard; protein; 234 AA.
DE  - Novel human secreted and transmembrane protein PRO1864.
PN    US2003049735-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 447
ID    ABM31773 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003068680-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 448
ID    ABM31163 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003068762-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 449
ID    ADB85809 standard; protein; 234 AA.
DE    Human secreted/transmembrane protein (PRO) #33.
PN    US2003054472-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 450
ID    ABM32078 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003068708-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 451
ID    ABM32383 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003068713-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 452
ID    ADB68266 standard; protein; 234 AA.
DE    Human PRO1864 protein.
PN    US2003065161-A1.
PD    03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 453
ID    ADB68073 standard; protein; 234 AA.
DE    Human PRO1864 protein.
PN    US2003060600-A1.
PD    27-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 454
ID    ABM31468 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003068761-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match          100.0%;    Score 1195;  DB 7;
      Best Local Similarity 100.0%;    Pred. No. 1.3e-131;    Length 234;
RESULT 455
ID    ABM30858 standard; protein; 234 AA.
DE    Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN    US2003068771-A1.
PD    10-APR-2003.
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PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 456
ID   ADB90890 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003083473-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 457
ID   ADC06970 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US2003060602-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 458
ID   ADC17149 standard; protein; 234 AA.
DE   Mammalian PRO polypeptide (SeqID 14).
PN   US2003065143-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 459
ID   ADC14847 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003073208-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 460
ID   ADC52342 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003138882-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 461
ID   ADD05539 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003087376-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 462
ID   ADD10351 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 463
ID   ADD11311 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 464
ID   ADD37104 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.

     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 465
ID   ADD36018 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003105298-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 466
ID   ADG01019 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 467
ID   ADG08572 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180793-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 468
ID   ADG02534 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207397-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 469
ID   ADG01241 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207399-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 470
ID   ADF95416 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207398-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 471
ID   ADF95193 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180795-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 472
ID   ADG12231 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207392-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
RESULT 473
ID   ADH24046 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180918-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         100.0%;  Score 1195;  DB 7;  Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.3e-131;
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RESULT 474
ID   ADH34072 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180858-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 475
ID   ADH29905 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180859-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 476
ID   ADH23876 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180919-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 477
ID   ADH08891 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003207395-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 478
ID   ADG85280 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180904-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 479
ID   ADH24556 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180907-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 480
ID   ADH37412 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181646-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 481
ID   ADH02001 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180837-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 482
ID   ADH37582 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181648-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 483
ID   ADG85620 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180905-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 484
ID   ADH24216 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180914-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 485
ID   ADH38510 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181643-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 486
ID   ADG83631 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180794-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 487
ID   ADH29439 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180860-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 488
ID   ADH27555 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180906-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 489
ID   ADH37752 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003181647-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 490
ID   ADH37929 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US2003181649-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 491
ID   ADH57349 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180920-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;
     Best Local Similarity   100.0%;   Score 1195; DB 7; Length 234;
                                       Pred. No. 1.3e-131;
RESULT 492
ID   ADH53491 standard; protein; 234 AA.
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DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181636-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 493
ID  ADH53661 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181641-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 494
ID  ADH51997 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181638-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 495
ID  ADH49852 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181639-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 496
ID  ADI25362 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181696-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 497
ID  ADH90155 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181698-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 498
ID  ADI25532 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181669-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 499
ID  ADH97706 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181672-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 500
ID  ADI03554 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181656-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 501
ID  ADI11911 standard; protein; 234 AA.
DE  Human PRO polypeptide #.

PN  US2003181686-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 502
ID  ADH89985 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181697-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 503
ID  ADH98386 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181707-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 504
ID  ADI11061 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181682-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 505
ID  ADI11571 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181684-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 506
ID  ADH98216 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181709-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 507
ID  ADH98556 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181708-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 508
ID  ADH98046 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181673-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 509
ID  ADI05034 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180848-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     100.0%;  Score 1195;  DB 7;  Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 510
ID  ADI03384 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181654-A1.
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PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 511
ID  ADI04779 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181657-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 512
ID  ADH78223 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181668-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 513
ID  ADI19577 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181676-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 514
ID  ADH90325 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181699-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 515
ID  ADI03044 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181653-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 516
ID  ADH77893 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181666-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 517
ID  ADH97876 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181674-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 518
ID  ADI01261 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003190669-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 519
ID  ADI01956 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181652-A1.
PD  25-SEP-2003.

PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 520
ID  ADI03214 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181655-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 521
ID  ADI11401 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181681-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 522
ID  ADI02303 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181650-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 523
ID  ADI11741 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181685-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 524
ID  ADI05378 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003190716-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 525
ID  ADH79450 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003191290-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 526
ID  ADI19407 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181675-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 527
ID  ADI05208 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003181677-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%;    Score 1195;  DB 7;   Length 234;
    Best Local Similarity  100.0%;  Pred. No. 1.3e-131;
RESULT 528
ID  ADH79620 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003191288-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
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Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 529
ID   ADI01446 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181678-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 530
ID   ADI01616 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181679-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 531
ID   ADI01786 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181680-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 532
ID   ADH79790 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003191289-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 533
ID   ADI04608 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003171550-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 534
ID   ADI02744 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181651-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 535
ID   ADH78063 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181667-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 536
ID   ADI25702 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181670-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 537
ID   ADI25872 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181671-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 7;  Length 234;


Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 538
ID   ADK65384 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003073821-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 539
ID   ADH98726 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003191284-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 540
ID   ADH79967 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003191287-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 541
ID   ADL32672 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207396-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 542
ID   ADM30206 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003073813-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 543
ID   ADL93698 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003040013-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 7;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 544
ID   ADC52152 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003130483-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 545
ID   ADE41312 standard; protein; 234 AA.
DE   Human secreted/transmembrane PRO polypeptide #31.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 546
ID   ADE74203 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003211572-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match             100.0%;  Score 1195;  DB 8;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.3e-131;
RESULT 547
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ID   ADE74815 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003211574-A1.
PD   13-NOV-2003.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 548
ID   ADF96028 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003215909-A1.
PD   20-NOV-2003.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 549
ID   ADG04299 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003215912-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 550
ID   ADG00459 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003215911-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 551
ID   ADH06584 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180852-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 552
ID   ADH06414 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180853-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 553
ID   ADG68835 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180855-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 554
ID   ADH27725 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180912-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 555
ID   ADH25066 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180913-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 556
ID   ADH33698 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181645-A1.

PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 557
ID   ADG82715 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003215910-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 558
ID   ADH02341 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180839-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 559
ID   ADH07948 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180845-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 560
ID   ADG69345 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180846-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 561
ID   ADH39166 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180917-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 562
ID   ADH25996 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003068770-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 563
ID   ADG83906 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003180842-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 564
ID   ADG85450 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003164848-A1.
PD   04-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;

RESULT 565
ID   ADH06244 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180854-A1.
PD   25-SEP-2003.

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PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 566
ID  ADH30074 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180856-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 567
ID  ADH24386 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180910-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 568
ID  ADH32965 standard; protein; 234 AA.
DE  Human PRO polypeptide #33.
PN  US2003068768-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 569
ID  ADG69515 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180844-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 570
ID  ADH07778 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180851-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 571
ID  ADH85790 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180861-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 572
ID  ADH39336 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180916-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 573
ID  ADH33528 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181637-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 574
ID  ADH33868 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003181644-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.

    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 575
ID  ADH01078 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003180038-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 576
ID  ADG69685 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180843-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 577
ID  ADH02171 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003180841-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 578
ID  ADG69175 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180847-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 579
ID  ADG85960 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180862-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 580
ID  ADH24896 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180909-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 581
ID  ADH39513 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180915-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 582
ID  ADH02511 standard; protein; 234 AA.
DE  Human PRO polypeptide #7.
PN  US2003180840-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
    Best Local Similarity      100.0%;   Pred. No. 1.3e-131;
RESULT 583
ID  ADG69005 standard; protein; 234 AA.
DE  Novel human secreted and transmembrane protein PRO1864.
PN  US2003180849-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match                100.0%;   Score 1195;  DB 8;  Length 234;
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        Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 584
ID   ADH07608 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180850-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 585
ID   ADG86130 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180863-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 586
ID   ADH24726 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180908-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 587
ID   ADH25774 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180911-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 588
ID   ADH38340 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180922-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 589
ID   ADH57179 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181642-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 590
ID   ADH43495 standard; protein; 234 AA.
DE   Human PRO polypeptide #31.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 591
ID   ADH52167 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180921-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 592
ID   ADH49533 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180857-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;

RESULT 593
ID   ADH90495 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181700-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 594
ID   ADI11231 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181683-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 595
ID   ADH98896 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003190698-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 596
ID   ADI02126 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003190699-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 597
ID   ADH90665 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181701-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 598
ID   ADJ54704 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2004023321-A1.
PD   05-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 599
ID   ADJ98540 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003187197-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 600
ID   ADJ98710 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003187228-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 601
ID   ADH78869 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181703-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;   Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-131;
RESULT 602
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ID   ADJ99103 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003186408-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 603
ID   ADJ99273 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003187196-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 604
ID   ADJ98891 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003187242-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 605
ID   ADH79039 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181702-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 606
ID   ADK00899 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003186407-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 607
ID   ADK14420 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003187229-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 608
ID   ADK82840 standard; protein; 234 AA.
DE   Human PRO polypeptide #31.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 609
ID   ADJ64475 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2004038337-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 610
ID   ADM31371 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2004048334-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 611
ID   ADM36418 standard; protein; 234 AA.

DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2004053358-A1.
PD   18-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 612
ID   ADM40223 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2004048335-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 613
ID   ADM80869 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2004058411-A1.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 614
ID   ADL91873 standard; protein; 234 AA.
DE   Human PRO1864 protein SEQ ID NO:94.
PN   WO2004024076-A2.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 615
ID   ADN37831 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2004091959-A1.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 8; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.3e-131;
RESULT 616
ID   AAM41716 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 6647.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   100.0%; Score 1195; DB 4; Length 238;
     Best Local Similarity   100.0%; Pred. No. 1.4e-131;
RESULT 617
ID   AAM41715 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 6646.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   100.0%; Score 1195; DB 4; Length 238;
     Best Local Similarity   100.0%; Pred. No. 1.4e-131;
RESULT 618
ID   ABP75508 standard; protein; 238 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 692.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   100.0%; Score 1195; DB 6; Length 238;
     Best Local Similarity   100.0%; Pred. No. 1.4e-131;
RESULT 619
ID   ABR58404 standard; protein; 234 AA.
DE   Human NOV19b.
PN   WO2003029423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   99.4%; Score 1188; DB 6; Length 234;
     Best Local Similarity   99.6%; Pred. No. 8.9e-131;
RESULT 620
ID   AAM39930 standard; protein; 216 AA.
DE   Human polypeptide SEQ ID NO 3075.

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PN  WO200153312-A1.
PD  26-JUL-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match         91.8%;  Score 1097;  DB 4;  Length 216;
    Best Local Similarity  92.3%;  Pred. No. 4.1e-120;
RESULT 621
ID  ABB90287 standard; protein; 201 AA.
DE  Human polypeptide SEQ ID NO 2663.
PN  WO200190304-A2.
PD  29-NOV-2001.
PA  (HUMA-) HUMAN GENOME SCI INC.
    Query Match         85.7%;  Score 1024;  DB 5;  Length 201;
    Best Local Similarity  100.0%;  Pred. No. 1.4e-111;
RESULT 622
ID  ABR58403 standard; protein; 198 AA.
DE  Human NOV19a.
PN  WO2003029423-A2.
PD  10-APR-2003.
PA  (CURA-) CURAGEN CORP.
    Query Match         82.4%;  Score 985;  DB 6;  Length 198;
    Best Local Similarity  84.6%;  Pred. No. 5.4e-107;
RESULT 623
ID  AAU30250 standard; protein; 283 AA.
DE  Novel human secreted protein #741.
PN  WO200179449-A2.
PD  25-OCT-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match         65.0%;  Score 777;  DB 4;  Length 283;
    Best Local Similarity  72.5%;  Pred. No. 2.6e-82;
RESULT 624
ID  ADB64413 standard; protein; 176 AA.
DE  Human protein encoded by clone FEBRA20007820.
PN  EP1308459-A2.
PD  07-MAY-2003.
PA  (HELI-) HELIX RES INST.
PA  (REAS-) RES ASSOC BIOTECHNOLOGY.
    Query Match         56.0%;  Score 669.5;  DB 7;  Length 176;
    Best Local Similarity  87.5%;  Pred. No. 6e-70;
RESULT 625
ID  ADK36828 standard; protein; 146 AA.
DE  Novel human polypeptide SeqID8910.
PN  WO200216439-A2.
PD  28-FEB-2002.
PA  (HYSE-) HYSEQ INC.
    Query Match         55.6%;  Score 665;  DB 5;  Length 146;
    Best Local Similarity  91.0%;  Pred. No. 1.6e-69;
RESULT 626
ID  AAW25768 standard; protein; 445 AA.
DE  Human MLN 64.
PN  WO9706256-A2.
PD  20-FEB-1997.
PA  (INRM ) INST NAT SANTE & RECH MEDICALE.
PA  (CNRS ) CENT NAT RECH SCI.
PA  (UYPA-) UNIV PASTEUR LOUIS.
PA  (BRIM ) BRISTOL-MYERS SQUIBB CO.
    Query Match         55.6%;  Score 664;  DB 2;  Length 445;
    Best Local Similarity  56.2%;  Pred. No. 9.6e-69;
RESULT 627
ID  ABR47530 standard; protein; 445 AA.
DE  Breast cancer associated protein sequence SEQ ID NO:296.
PN  WO2003004989-A2.
PD  16-JAN-2003.
PA  (MILL-) MILLENIUM PHARM INC.
    Query Match         55.6%;  Score 664;  DB 6;  Length 445;
    Best Local Similarity  56.2%;  Pred. No. 9.6e-69;
RESULT 628
ID  ADH13184 standard; protein; 445 AA.
DE  Human malignant neoplasia-related protein SeqID33.
PN  EP1365034-A2.
PD  26-NOV-2003.
PA  (FARB ) BAYER AG.
    Query Match         55.6%;  Score 664;  DB 8;  Length 445;
    Best Local Similarity  56.2%;  Pred. No. 9.6e-69;

RESULT 629
ID  ABG05498 standard; protein; 534 AA.
DE  Novel human diagnostic protein #5489.
PN  WO200175067-A2.
PD  11-OCT-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match         52.3%;  Score 625;  DB 4;  Length 534;
    Best Local Similarity  48.9%;  Pred. No. 4.8e-64;
RESULT 630
ID  ABR69622 standard; protein; 412 AA.
DE  Human CGDD-22 protein.
PN  WO2003027263-A2.
PD  03-APR-2003.
PA  (INCY-) INCYTE GENOMICS INC.
    Query Match         48.4%;  Score 578;  DB 6;  Length 412;
    Best Local Similarity  58.3%;  Pred. No. 1.1e-58;
RESULT 631
ID  ABP75900 standard; protein; 111 AA.
DE  Human secretory polypeptide SPTM SEQ ID NO 1084.
PN  WO200283876-A2.
PD  24-OCT-2002.
PA  (INCY-) INCYTE GENOMICS INC.
    Query Match         33.9%;  Score 405.5;  DB 6;  Length 111;
    Best Local Similarity  73.7%;  Pred. No. 3.6e-39;
RESULT 632
ID  ABB59968 standard; protein; 580 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 6696.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match         28.7%;  Score 343;  DB 4;  Length 580;
    Best Local Similarity  37.8%;  Pred. No. 8e-31;
RESULT 633
ID  AAM90384 standard; protein; 70 AA.
DE  Human immune/haematopoietic antigen SEQ ID NO:17977.
PN  WO200157182-A2.
PD  09-AUG-2001.
PA  (HUMA-) HUMAN GENOME SCI INC.
    Query Match         26.9%;  Score 322;  DB 4;  Length 70;
    Best Local Similarity  98.4%;  Pred. No. 1.3e-29;
RESULT 634
ID  AAB96837 standard; protein; 424 AA.
DE  Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PN  FR2792651-A1.
PD  27-OCT-2000.
PA  (CNRS ) CNRS CENT NAT RECH SCI.
PA  (IFRE-) IFREMER INST FR RECH EXPL MER.
    Query Match         7.8%;  Score 93.5;  DB 4;  Length 424;
    Best Local Similarity  21.9%;  Pred. No. 0.12;
RESULT 635
ID  AAU03699 standard; protein; 373 AA.
DE  Group B Streptococcus antigenic protein, ID-176.
PN  WO200132882-A2.
PD  10-MAY-2001.
PA  (MICR-) MICROBIAL TECHNICS LTD.
    Query Match         7.6%;  Score 91;  DB 4;  Length 373;
    Best Local Similarity  25.7%;  Pred. No. 0.19;
RESULT 636
ID  ABP30317 standard; protein; 651 AA.
DE  Streptococcus polypeptide SEQ ID NO 9810.
PN  WO200234771-A2.
PD  02-MAY-2002.
PA  (CHIR-) CHIRON SPA.
PA  (GENO-) INST GENOMIC RES.
    Query Match         7.6%;  Score 91;  DB 5;  Length 651;
    Best Local Similarity  25.7%;  Pred. No. 0.42;
RESULT 637
ID  ABP29732 standard; protein; 654 AA.
DE  Streptococcus polypeptide SEQ ID NO 8640.
PN  WO200234771-A2.
PD  02-MAY-2002.
PA  (CHIR-) CHIRON SPA.
PA  (GENO-) INST GENOMIC RES.
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Query Match   7.6%;   Score 91;   DB 5;   Length 654;
Best Local Similarity 25.7%;   Pred. No. 0.42;
RESULT 638
ID ABP26469 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 2114.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match   7.6%;   Score 91;   DB 5;   Length 654;
Best Local Similarity 25.7%;   Pred. No. 0.42;
RESULT 639
ID AAG61678 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match   7.3%;   Score 87.5;   DB 3;   Length 155;
Best Local Similarity 21.4%;   Pred. No. 0.15;
RESULT 640
ID AAG59838 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match   7.3%;   Score 87.5;   DB 3;   Length 155;
Best Local Similarity 21.4%;   Pred. No. 0.15;
RESULT 641
ID AAB58945 standard; protein; 516 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.3%;   Score 87.5;   DB 3;   Length 516;
Best Local Similarity 25.2%;   Pred. No. 0.78;
RESULT 642
ID ADQ39266 standard; protein; 421 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 929.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.3%;   Score 87;   DB 8;   Length 421;
Best Local Similarity 23.7%;   Pred. No. 0.67;
RESULT 643
ID ADQ39263 standard; protein; 223 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 926.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 223;
Best Local Similarity 25.5%;   Pred. No. 0.42;
RESULT 644
ID ADQ39258 standard; protein; 285 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 921.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 285;
Best Local Similarity 25.5%;   Pred. No. 0.59;
RESULT 645
ID ADQ39262 standard; protein; 315 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 925.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 315;
Best Local Similarity 25.5%;   Pred. No. 0.68;
RESULT 646
ID ADQ39260 standard; protein; 323 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 923.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 323;
Best Local Similarity 25.5%;   Pred. No. 0.7;

RESULT 647
ID ADQ39261 standard; protein; 328 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 924.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 328;
Best Local Similarity 25.5%;   Pred. No. 0.71;
RESULT 648
ID ADQ39265 standard; protein; 338 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 928.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 338;
Best Local Similarity 25.5%;   Pred. No. 0.74;
RESULT 649
ID ADQ39267 standard; protein; 339 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 930.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 339;
Best Local Similarity 25.5%;   Pred. No. 0.75;
RESULT 650
ID ADE28099 standard; protein; 340 AA.
DE Human NTRAN protein - SEQ ID 4.
PN WO2003051902-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match   7.2%;   Score 85.5;   DB 7;   Length 340;
Best Local Similarity 25.5%;   Pred. No. 0.75;
RESULT 651
ID ADQ39269 standard; protein; 384 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 932.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 384;
Best Local Similarity 25.5%;   Pred. No. 0.75;
RESULT 652
ID ADQ39264 standard; protein; 390 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 927.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match   7.2%;   Score 85.5;   DB 8;   Length 390;
Best Local Similarity 25.5%;   Pred. No. 0.91;
RESULT 653
ID ABU26680 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #12207.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match   7.2%;   Score 85.5;   DB 6;   Length 396;
Best Local Similarity 21.0%;   Pred. No. 0.93;
RESULT 654
ID AAW13575 standard; protein; 438 AA.
DE Batten disease polypeptide CLN3.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match   7.2%;   Score 85.5;   DB 2;   Length 438;
Best Local Similarity 25.5%;   Pred. No. 1.1;
RESULT 655
ID AAW13589 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L204.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match   7.2%;   Score 85.5;   DB 2;   Length 438;
Best Local Similarity 25.5%;

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          Best Local Similarity  24.8%;  Pred. No. 1.1;
RESULT 656
ID   AAW13582 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L46.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match  7.2%;  Score 85.5;  DB 2;  Length 438;
     Best Local Similarity  25.5%;  Pred. No. 1.1;
RESULT 657
ID   AAW13577 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L39.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match  7.2%;  Score 85.5;  DB 2;  Length 438;
     Best Local Similarity  25.5%;  Pred. No. 1.1;
RESULT 658
ID   ADQ96392 standard; protein; 438 AA.
DE   T cell activation associated protein #285.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match  7.2%;  Score 85.5;  DB 8;  Length 438;
     Best Local Similarity  25.5%;  Pred. No. 1.1;
RESULT 659
ID   ADQ39268 standard; protein; 438 AA.
DB   Human myocardial infarction-associated gene derived protein, SEQ ID 931.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match  7.2%;  Score 85.5;  DB 2;  Length 438;
     Best Local Similarity  25.5%;  Pred. No. 1.1;
RESULT 660
ID   ADN63244 standard; protein; 440 AA.
DE   Human NOV43a variant.
PN   WO2003029424-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match  7.2%;  Score 85.5;  DB 6;  Length 440;
     Best Local Similarity  25.2%;  Pred. No. 1.1;
RESULT 661
ID   ADN63244 standard; protein; 440 AA.
DE   Human NOV43a variant.
PN   US2004038223-A1.
PD   26-FEB-2004.
PA   (SMIT/) SMITHSON G.
PA   (MILL/) MILLET I.
PA   (PEYM/) PEYMAN J A.
PA   (KEKU/) KEKUDA R.
PA   (JUUJ/) JU J.
PA   (LILL/) LI L.
PA   (GUOX/) GUO X.
PA   (PATT/) PATTURAJAN M.
PA   (SPYT/) SPYTEK K A.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (MALY/) MALYANKAR U M.
PA   (ORTT/) ORT T.
PA   (GORM/) GORMAN L.
PA   (ZERH/) ZERHUSEN B D.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (CATT/) CATTERTON E.
PA   (JIWW/) JI W.
PA   (MILL/) MILLER C B.
PA   (RAST/) RASTELLI L.
PA   (STON/) STONE D J.
PA   (PENA/) PENA C E A.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (ROTH/) ROTHENBERG M E.
PA   (LEAC/) LEACH M D.
PA   (AGEE/) AGEE M L.
PA   (BERG/) BERGHS C.
PA   (DIPI/) DIPIPPO V A.
PA   (EISE/) EISEN A.
PA   (GANG/) GANGOLLI E A.
PA   (RIEG/) RIEGER D K.
PA   (SPAD/) SPADERNA S K.
     Query Match  7.2%;  Score 85.5;  DB 8;  Length 440;
     Best Local Similarity  25.2%;  Pred. No. 1.1;
RESULT 662
ID   ADN62985 standard; protein; 440 AA.
DE   Human NOV43a.
PN   US2004038223-A1.
PD   26-FEB-2004.
PA   (SMIT/) SMITHSON G.
PA   (MILL/) MILLET I.
PA   (PEYM/) PEYMAN J A.
PA   (KEKU/) KEKUDA R.
PA   (JUUJ/) JU J.
PA   (LILL/) LI L.
PA   (GUOX/) GUO X.
PA   (PATT/) PATTURAJAN M.
PA   (SPYT/) SPYTEK K A.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (MALY/) MALYANKAR U M.
PA   (ORTT/) ORT T.
PA   (GORM/) GORMAN L.
PA   (ZERH/) ZERHUSEN B D.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (CATT/) CATTERTON E.
PA   (JIWW/) JI W.
PA   (MILL/) MILLER C B.
PA   (RAST/) RASTELLI L.
PA   (STON/) STONE D J.
PA   (PENA/) PENA C E A.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (ROTH/) ROTHENBERG M E.
PA   (LEAC/) LEACH M D.
PA   (AGEE/) AGEE M L.
PA   (BERG/) BERGHS C.
PA   (DIPI/) DIPIPPO V A.
PA   (EISE/) EISEN A.
PA   (GANG/) GANGOLLI E A.
PA   (RIEG/) RIEGER D K.
PA   (SPAD/) SPADERNA S K.
     Query Match  7.2%;  Score 85.5;  DB 8;  Length 440;
     Best Local Similarity  25.2%;  Pred. No. 1.1;
RESULT 663
ID   AAW13593 standard; protein; 467 AA.
DE   Batten disease CLN3 mutant protein in family L61.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match  7.2%;  Score 85.5;  DB 2;  Length 467;
     Best Local Similarity  25.5%;  Pred. No. 1.2;
RESULT 664
ID   ABB89640 standard; protein; 473 AA.
DE   Human polypeptide SEQ ID NO 2016.
PN   WO20190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match  7.2%;  Score 85.5;  DB 5;  Length 473;
     Best Local Similarity  25.2%;  Pred. No. 1.2;
RESULT 665
ID   ADQ18055 standard; protein; 473 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN   WO2004048938-A2.
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PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match   7.2%;   Score 85.5;   DB 8;   Length 473;
     Best Local Similarity   25.2%;   Pred. No. 1.2;
RESULT 666
ID   ABU40544 standard; protein; 500 AA.
DE   Protein encoded by Prokaryotic essential gene #26071.
PN   WO20027183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.2%;   Score 85.5;   DB 6;   Length 500;
     Best Local Similarity   26.0%;   Pred. No. 1.3;
RESULT 667
ID   ABU33210 standard; protein; 430 AA.
DE   Protein encoded by Prokaryotic essential gene #18737.
PN   WO20027183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   7.1%;   Score 84.5;   DB 6;   Length 430;
     Best Local Similarity   25.5%;   Pred. No. 1.4;
RESULT 668
ID   AAW13588 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L10.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match   7.1%;   Score 84.5;   DB 2;   Length 438;
     Best Local Similarity   24.8%;   Pred. No. 1.4;
RESULT 669
ID   AAG16921 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   7.0%;   Score 83.5;   DB 3;   Length 322;
     Best Local Similarity   33.7%;   Pred. No. 1.2;
RESULT 670
ID   ABG21285 standard; protein; 472 AA.
DE   Novel human diagnostic protein #21276.
PN   WO20017506-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.0%;   Score 83.5;   DB 4;   Length 472;
     Best Local Similarity   20.1%;   Pred. No. 2;
RESULT 671
ID   ABU35608 standard; protein; 239 AA.
DE   Protein encoded by Prokaryotic essential gene #21135.
PN   WO20027183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.9%;   Score 82.5;   DB 6;   Length 239;
     Best Local Similarity   21.7%;   Pred. No. 1;
RESULT 672
ID   AAW13590 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L216.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match   6.9%;   Score 82.5;   DB 2;   Length 438;
     Best Local Similarity   24.8%;   Pred. No. 2.4;
RESULT 673
ID   ADB85263 standard; protein; 589 AA.
DE   Mouse RNAi homologue SEQ ID NO:144.
PN   EP1284297-A2.
PD   19-FEB-2003.
PA   (WARN) WARNER LAMBERT CO.
     Query Match   6.9%;   Score 82;   DB 7;   Length 589;
     Best Local Similarity   19.5%;   Pred. No. 4.2;
RESULT 674
ID   AAW13586 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L285.
PN   WO9708308-A1.

PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match   6.8%;   Score 81.5;   DB 2;   Length 438;
     Best Local Similarity   24.8%;   Pred. No. 3.2;
RESULT 675
ID   AAB92924 standard; protein; 519 AA.
DE   Human protein sequence SEQ ID NO:11574.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
     Query Match   6.8%;   Score 81.5;   DB 4;   Length 519;
     Best Local Similarity   22.6%;   Pred. No. 4;
RESULT 676
ID   ADE28193 standard; protein; 577 AA.
DE   Human MDDT protein - SEQ ID 43.
PN   WO200304152-A2.
PD   05-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   6.8%;   Score 81.5;   DB 7;   Length 577;
     Best Local Similarity   22.6%;   Pred. No. 4.6;
RESULT 677
ID   ADN23155 standard; protein; 529 AA.
DE   Bacterial polypeptide #5808.
PN   US200233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.8%;   Score 81;   DB 8;   Length 529;
     Best Local Similarity   23.1%;   Pred. No. 4.7;
RESULT 678
ID   ADN23156 standard; protein; 529 AA.
DE   Bacterial polypeptide #5809.
PN   US200233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.8%;   Score 81;   DB 8;   Length 529;
     Best Local Similarity   23.1%;   Pred. No. 4.7;
RESULT 679
ID   AAG53771 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68491.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.7%;   Score 80.5;   DB 3;   Length 322;
     Best Local Similarity   32.7%;   Pred. No. 2.7;
RESULT 680
ID   AAG25639 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 29783.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.7%;   Score 80.5;   DB 3;   Length 322;
     Best Local Similarity   32.7%;   Pred. No. 2.7;
RESULT 681
ID   AAG53746 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68457.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.7%;   Score 80.5;   DB 3;   Length 322;
     Best Local Similarity   32.7%;   Pred. No. 2.7;
RESULT 682
ID   ABO63194 standard; protein; 350 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9711.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   6.7%;   Score 80.5;   DB 7;   Length 350;

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     Best Local Similarity    31.8%;    Pred. No.  3;
RESULT 683
ID   ABB48552 standard; protein; 463 AA.
DE   Listeria monocytogenes protein #1256.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST PASTEUR.
     Query Match             6.7%;    Score 80.5; DB 5;  Length 463;
     Best Local Similarity   19.0%;    Pred. No.  4.5;
RESULT 684
ID   ABU33036 standard; protein; 463 AA.
DE   Protein encoded by Prokaryotic essential gene #18563.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.7%;    Score 80.5; DB 6;  Length 463;
     Best Local Similarity   19.0%;    Pred. No.  4.5;
RESULT 685
ID   ADD43870 standard; protein; 536 AA.
DE   Chlamydia trachomatis immunogenic protein, SEQ ID No 165.
PN   WO2003049762-A2.
PD   19-JUN-2003.
PA   (CHIR-) CHIRON SPA.
     Query Match             6.7%;    Score 80.5; DB 7;  Length 536;
     Best Local Similarity   25.2%;    Pred. No.  5.5;
RESULT 686
ID   ADC42920 standard; protein; 891 AA.
DE   Vaccinia Virus Major Core protein P4a precursor.
PN   WO2003017943-A2.
PD   06-MAR-2003.
PA   (MYRI-) MYRIAD GENETICS INC.
     Query Match             6.7%;    Score 80.5; DB 7;  Length 891;
     Best Local Similarity   23.3%;    Pred. No.  11;
RESULT 687
ID   ABB92830 standard; protein; 1780 AA.
DE   Herbicidally active polypeptide SEQ ID NO 2041.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB ) BAYER AG.
     Query Match             6.7%;    Score 80.5; DB 5;  Length 1780;
     Best Local Similarity   20.8%;    Pred. No.  29;
RESULT 688
ID   AAB54399 standard; protein; 144 AA.
DE   Human pancreatic cancer antigen protein sequence SEQ ID NO:851.
PN   WO200055320-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             6.7%;    Score 80; DB 3;  Length 144;
     Best Local Similarity   25.4%;    Pred. No.  1;
RESULT 689
ID   AAM39952 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 3097.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             6.7%;    Score 80; DB 7;  Length 238;
     Best Local Similarity   22.5%;    Pred. No.  2;
RESULT 690
ID   ADM04473 standard; protein; 238 AA.
DE   Human protein of the invention SEQ ID NO:3158.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (REAS-) RBS ASSOC BIOTECHNOLOGY.
     Query Match             6.7%;    Score 80; DB 4;  Length 238;
     Best Local Similarity   22.5%;    Pred. No.  2;
RESULT 691
ID   AAM41738 standard; protein; 249 AA.
DE   Human polypeptide SEQ ID NO 6669.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             6.7%;    Score 80; DB 4;  Length 249;
     Best Local Similarity   22.5%;    Pred. No.  2.2;

RESULT 692
ID   AAR77844 standard; protein; 309 AA.
DE   Molasses toxicity resistance protein RTM1.
PN   WO9514774-A2.
PD   01-JUN-1995.
PA   (CNRS ) CENT NAT RECH SCI.
     Query Match             6.7%;    Score 80; DB 2;  Length 309;
     Best Local Similarity   28.0%;    Pred. No.  2.9;
RESULT 693
ID   ABM67388 standard; protein; 330 AA.
DE   Photorhabdus luminescens protein sequence #485.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             6.7%;    Score 80; DB 6;  Length 330;
     Best Local Similarity   24.6%;    Pred. No.  3.2;
RESULT 694
ID   AAE03831 standard; protein; 360 AA.
DE   Human gene 14 encoded secreted protein HDQFN31, SEQ ID NO: 77.
PN   WO200136440-A1.
PD   25-MAY-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             6.7%;    Score 80; DB 4;  Length 360;
     Best Local Similarity   22.5%;    Pred. No.  3.6;
RESULT 695
ID   ABG64559 standard; protein; 360 AA.
DE   Human albumin fusion protein #1234.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             6.7%;    Score 80; DB 5;  Length 360;
     Best Local Similarity   22.5%;    Pred. No.  3.6;
RESULT 696
ID   ADL77826 standard; protein; 360 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1308.
PN   US2004010134-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
     Query Match             6.7%;    Score 80; DB 8;  Length 360;
     Best Local Similarity   22.5%;    Pred. No.  3.6;
RESULT 697
ID   ABU25554 standard; protein; 365 AA.
DE   Protein encoded by Prokaryotic essential gene #11081.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.7%;    Score 79.5; DB 6;  Length 365;
     Best Local Similarity   21.2%;    Pred. No.  4.2;
RESULT 698
ID   AAR58703 standard; protein; 406 AA.
DE   HCMV IE-exon-4 subunit.
PN   WO9417810-A1.
PD   18-AUG-1994.
PA   (WIST-) WISTAR INST ANATOMY & BIOLOGY.
     Query Match             6.7%;    Score 79.5; DB 2;  Length 406;
     Best Local Similarity   19.3%;    Pred. No.  4.9;
RESULT 699
ID   AAW27275 standard; protein; 406 AA.
DE   Human cytomegalovirus immediate-early exon 4 product.
PN   WO9740165-A1.
PD   30-OCT-1997.
PA   (WIST-) WISTAR INST ANATOMY & BIOLOGY.
     Query Match             6.7%;    Score 79.5; DB 2;  Length 406;
     Best Local Similarity   19.3%;    Pred. No.  4.9;
RESULT 700
ID   ABB58483 standard; protein; 638 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 2241.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
     Query Match             6.7%;    Score 79.5; DB 4;  Length 638;
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Best Local Similarity 20.5%; Pred. No. 9.1;
RESULT 701
ID AAB13277 standard; protein; 723 AA.
DE Human transporters and ion channels (TRICH)-4.
PN WO200177174-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 79.5; DB 5; Length 723;
Best Local Similarity 18.0%; Pred. No. 11;
RESULT 702
ID ADL12774 standard; protein; 723 AA.
DE Human steroid-induced C3A liver cell protein #80.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 79.5; DB 8; Length 723;
Best Local Similarity 18.0%; Pred. No. 11;
RESULT 703
ID AAW20696 standard; protein; 121 AA.
DE H. Pylori secreted or periplasmic protein 05ae20220orf50.
PN WO640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.6%; Score 79; DB 2; Length 121;
Best Local Similarity 21.4%; Pred. No. 1;
RESULT 704
ID ABB60462 standard; protein; 323 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8178.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.6%; Score 79; DB 4; Length 323;
Best Local Similarity 18.8%; Pred. No. 4.1;
RESULT 705
ID ABR58610 standard; protein; 1531 AA.
DE Human cancer related protein SEQ ID NO:267.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.6%; Score 79; DB 6; Length 1531;
Best Local Similarity 24.3%; Pred. No. 35;
RESULT 706
ID ADE31753 standard; protein; 1531 AA.
DE Human 59590 protein #SEQ ID 110.
PN WO2003065984-A2.
PD 14-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.6%; Score 79; DB 7; Length 1531;
Best Local Similarity 24.3%; Pred. No. 35;
RESULT 707
ID ABU62069 standard; protein; 1597 AA.
DE Mouse heart alpha-kinase (HK).
PN US2002217205-A1.
PD 28-NOV-2002.
PA (RYAZ/) RYAZANOV A.
Query Match 6.6%; Score 79; DB 6; Length 1597;
Best Local Similarity 24.3%; Pred. No. 37;
RESULT 708
ID ABU62070 standard; protein; 1597 AA.
DE Human heart alpha-kinase (HK).
PN US2002217205-A1.
PD 28-NOV-2002.
PA (RYAZ/) RYAZANOV A.
Query Match 6.6%; Score 79; DB 6; Length 1597;
Best Local Similarity 24.3%; Pred. No. 37;
RESULT 709
ID ABO55689 standard; protein; 135 AA.
DE Human genome derived single exon protein #1923.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.

Query Match 6.6%; Score 78.5; DB 8; Length 135;
Best Local Similarity 59.4%; Pred. No. 1.4;
RESULT 710
ID ADB10816 standard; protein; 228 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:4244.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 6.6%; Score 78.5; DB 6; Length 228;
Best Local Similarity 22.5%; Pred. No. 2.9;
RESULT 711
ID ABU36298 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #21825.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.6%; Score 78.5; DB 6; Length 239;
Best Local Similarity 23.4%; Pred. No. 3.1;
RESULT 712
ID ADJ27174 standard; protein; 626 AA.
DE Human TRICH-6, SEQ ID 6.
PN WO2004013293-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 626;
Best Local Similarity 18.0%; Pred. No. 12;
RESULT 713
ID ABM84879 standard; protein; 648 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5128.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 648;
Best Local Similarity 18.0%; Pred. No. 12;
RESULT 714
ID ABM84877 standard; protein; 668 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5126.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 668;
Best Local Similarity 18.0%; Pred. No. 13;
RESULT 715
ID ABP29904 standard; protein; 669 AA.
DE Streptococcus polypeptide SEQ ID NO 8984.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.6%; Score 78.5; DB 5; Length 669;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 716
ID ABP28724 standard; protein; 669 AA.
DE Streptococcus polypeptide SEQ ID NO 6624.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.6%; Score 78.5; DB 5; Length 669;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 717
ID ADI21047 standard; protein; 703 AA.
DE Novel human protein #22.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 78.5; DB 7; Length 703;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 718
ID ABM84882 standard; protein; 711 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5131.
PN WO2004023973-A2.
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 711;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 719
ID ABP52105 standard; protein; 723 AA.
DE Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 6.6%; Score 78.5; DB 5; Length 723;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 720
ID ADQ97094 standard; protein; 723 AA.
DE Human cancer associated sequence HP1-10-005, SEQ ID 70.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 78.5; DB 8; Length 723;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 721
ID AAB02437 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 722
ID AAE02441 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein mutant K545R.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 723
ID AAE02442 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein mutant D667N.
PN WO200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 724
ID AAG67163 standard; protein; 766 AA.
DE Amino acid sequence of a human 33894 transporter polypeptide.
PN WO200164875-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 725
ID AAG79246 standard; protein; 766 AA.
DE Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.
PN WO200173018-A2.
PD 04-OCT-2001.
PA (MERE) MERCK PATENT GMBH.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 726
ID ABB98345 standard; protein; 766 AA.
DE Human ABC transporter ABCB9 SEQ ID NO 6.
PN WO200264781-A2.
PD 22-AUG-2002.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 727
ID AAE21170 standard; protein; 766 AA.
DE Human TRICH-14 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 728
ID ADQ97096 standard; protein; 766 AA.
DE Human cancer associated sequence HP2-10-005, SEQ ID 72.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 78.5; DB 8; Length 766;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 729
ID AAG20805 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
PN EP103405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 78; DB 3; Length 377;
Best Local Similarity 23.8%; Pred. No. 6.6;
RESULT 730
ID AAG20804 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
PN EP103405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 78; DB 3; Length 442;
Best Local Similarity 23.8%; Pred. No. 8.2;
RESULT 731
ID AAU35545 standard; protein; 471 AA.
DE Haemophilus influenzae cellular proliferation protein #186.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 78; DB 4; Length 471;
Best Local Similarity 25.0%; Pred. No. 9;
RESULT 732
ID ABU30411 standard; protein; 471 AA.
DE Protein encoded by Prokaryotic essential gene #15938.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 78; DB 6; Length 471;
Best Local Similarity 25.0%; Pred. No. 9;
RESULT 733
ID AAG20803 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
PN EP103405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 78; DB 3; Length 489;
Best Local Similarity 23.8%; Pred. No. 9.5;
RESULT 734
ID ABB49039 standard; protein; 269 AA.
DE Listeria monocytogenes protein #1743.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.5%; Score 77.5; DB 5; Length 269;
Best Local Similarity 22.0%; Pred. No. 4.7;
RESULT 735
ID ABG17374 standard; protein; 280 AA.
DE Novel human diagnostic protein #17365.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 77.5; DB 4; Length 280;
Best Local Similarity 21.9%; Pred. No. 5;
RESULT 736
ID ABO00771 standard; protein; 280 AA.
DE Polypeptide encoded by novel human contig #22.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 77.5; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 5;
RESULT 737
ID ABU48889 standard; protein; 327 AA.

DE   Protein encoded by Prokaryotic essential gene #34416.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.5%;   Score 77.5;   DB 6;   Length 327;
     Best Local Similarity 24.8%;   Pred. No. 6.2;
RESULT 738
ID   AAW13576 standard; protein; 438 AA.
DE   Mouse Batten disease polypeptide CLN3 homologue.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
     Query Match   6.5%;   Score 77.5;   DB 2;   Length 438;
     Best Local Similarity 27.6%;   Pred. No. 9.3;
RESULT 739
ID   ADS42965 standard; protein; 491 AA.
DE   Bacterial polypeptide #21395.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.5%;   Score 77.5;   DB 8;   Length 491;
     Best Local Similarity 22.6%;   Pred. No. 11;
RESULT 740
ID   ADC42919 standard; protein; 892 AA.
DE   Variola smallpox virus A1OL.
PN   WO2003017943-A2.
PD   06-MAR-2003.
PA   (MYRI-) MYRIAD GENETICS INC.
     Query Match   6.5%;   Score 77.5;   DB 7;   Length 892;
     Best Local Similarity 22.7%;   Pred. No. 25;
RESULT 741
ID   AAR88413 standard; protein; 353 AA.
DE   High-affinity melatonin-1a receptor.
PN   WO9803549-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
     Query Match   6.5%;   Score 77.5;   DB 2;   Length 353;
     Best Local Similarity 22.1%;   Pred. No. 7.9;
RESULT 742
ID   AAW23958 standard; protein; 353 AA.
DE   Mouse melatonin 1a receptor.
PN   WO9803549-A1.
PD   29-JAN-1998.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   6.4%;   Score 77;   DB 2;   Length 353;
     Best Local Similarity 22.1%;   Pred. No. 7.9;
RESULT 743
ID   ABB07571 standard; protein; 353 AA.
DE   Mouse melatonin 1a (Mella) receptor.
PN   US6326526-B1.
PD   04-DEC-2001.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   6.4%;   Score 77;   DB 5;   Length 353;
     Best Local Similarity 22.1%;   Pred. No. 7.9;
RESULT 744
ID   ADO29553 standard; protein; 353 AA.
DE   Mouse GPCR MTNR1A, SEQ ID NO:655.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match   6.4%;   Score 77;   DB 8;   Length 353;
     Best Local Similarity 22.1%;   Pred. No. 7.9;
RESULT 745
ID   ADM25403 standard; protein; 383 AA.
DE   Hyperthermophile Methanopyrus kandleri protein #9.
PN   WO2003076575-A2.
PD   18-SEP-2003.

PA   (FIDE-) FIDELITY SYSTEMS INC.
PA   (MALY/) MALYKH A.
     Query Match   6.4%;   Score 77;   DB 7;   Length 383;
     Best Local Similarity 24.8%;   Pred. No. 8.9;
RESULT 746
ID   ADQ95948 standard; protein; 490 AA.
DE   T cell activation associated protein #63.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match   6.4%;   Score 77;   DB 8;   Length 490;
     Best Local Similarity 19.5%;   Pred. No. 12;
RESULT 747
ID   ADQ96002 standard; protein; 490 AA.
DE   T cell activation associated protein #90.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match   6.4%;   Score 77;   DB 8;   Length 490;
     Best Local Similarity 19.5%;   Pred. No. 12;
RESULT 748
ID   AAG42521 standard; protein; 648 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   6.4%;   Score 77;   DB 3;   Length 648;
     Best Local Similarity 20.4%;   Pred. No. 18;
RESULT 749
ID   ABU16172 standard; protein; 650 AA.
DE   Protein encoded by Prokaryotic essential gene #1699.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.4%;   Score 77;   DB 6;   Length 650;
     Best Local Similarity 27.5%;   Pred. No. 18;
RESULT 750
ID   ABM72713 standard; protein; 650 AA.
DE   Staphylococcus aureus protein #1953.
PN   WO20294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match   6.4%;   Score 77;   DB 6;   Length 650;
     Best Local Similarity 27.5%;   Pred. No. 18;
RESULT 751
ID   AAG42520 standard; protein; 690 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   6.4%;   Score 77;   DB 3;   Length 690;
     Best Local Similarity 20.4%;   Pred. No. 20;
RESULT 752
ID   AAG42519 standard; protein; 728 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   6.4%;   Score 77;   DB 3;   Length 728;
     Best Local Similarity 20.4%;   Pred. No. 22;
RESULT 753
ID   AAG42549 standard; protein; 805 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39287.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   6.4%;   Score 77;   DB 3;   Length 805;
     Best Local Similarity 20.4%;   Pred. No. 25;
RESULT 754
ID   AAG32548 standard; protein; 847 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   6.4%;   Score 77;   DB 3;   Length 847;
     Best Local Similarity 20.4%;   Pred. No. 27;
RESULT 755
ID   AAG32547 standard; protein; 991 AA.

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DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
PN   EP1033405-A2.
PD   06-SEP-2000.
       Query Match            6.4%;    Score 77;   DB 3;   Length 991;
       Best Local Similarity  20.4%;   Pred. No. 33;
RESULT 756
ID   ABP52133 standard; protein; 1025 AA.
DE   Plasmodium falciparummultidrug resistance protein SEQ ID NO:85.
PN   EP1217066-A1.
PD   26-JUN-2002.
PA   (UYGE-) UNIV GENT.
       Query Match            6.4%;    Score 77;   DB 5;   Length 1025;
       Best Local Similarity  20.6%;   Pred. No. 35;
RESULT 757
ID   AAG42381 standard; protein; 1047 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
PN   EP1033405-A2.
PD   06-SEP-2000.
       Query Match            6.4%;    Score 77;   DB 3;   Length 1047;
       Best Local Similarity  20.4%;   Pred. No. 36;
RESULT 758
ID   AAG42380 standard; protein; 1191 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
PN   EP1033405-A2.
PD   06-SEP-2000.
       Query Match            6.4%;    Score 77;   DB 3;   Length 1191;
       Best Local Similarity  20.4%;   Pred. No. 43;
RESULT 759
ID   AAG42379 standard; protein; 1202 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
PN   EP1033405-A2.
PD   06-SEP-2000.
       Query Match            6.4%;    Score 77;   DB 3;   Length 1202;
       Best Local Similarity  20.4%;   Pred. No. 43;
RESULT 760
ID   AAR29527 standard; protein; 2510 AA.
DE   HCV antigen T7N1-30.
PN   EP518313-A2.
PD   16-DEC-1992.
PA   (MITU ) MITSUBISHI KASEI CORP.
       Query Match            6.4%;    Score 77;   DB 2;   Length 2510;
       Best Local Similarity  22.5%;   Pred. No. 1.2e+02;
RESULT 761
ID   ADF74966 standard; protein; 249 AA.
DE   Human 164-1h protein (SeqID 25).
PN   WO2003097686-A1.
PD   27-NOV-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
       Query Match            6.4%;    Score 76.5;   DB 7;   Length 249;
       Best Local Similarity  28.5%;   Pred. No. 12;
RESULT 762
ID   ADC01137 standard; protein; 278 AA.
DE   Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1181.
PN   JP2002355074-A.
PD   10-DEC-2002.
PA   (UYTS-) UNIV TSUKUBA.
       Query Match            6.4%;    Score 76.5;   DB 7;   Length 278;
       Best Local Similarity  28.5%;   Pred. No. 6.5;
RESULT 763
ID   AB065827 standard; protein; 435 AA.
DE   Klebsiella pneumoniae polypeptide seqid 12344.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
       Query Match            6.4%;    Score 76.5;   DB 7;   Length 435;
       Best Local Similarity  21.8%;   Pred. No. 12;
RESULT 764
ID   ADF74969 standard; protein; 481 AA.
DE   Human 164-1b protein (SeqID 28).
PN   WO2003097686-A1.
PD   27-NOV-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.
       Query Match            6.4%;    Score 76.5;   DB 8;   Length 481;
       Best Local Similarity  23.3%;   Pred. No. 14;
RESULT 765
ID   AAR90765 standard; protein; 494 AA.
DE   Human K+ channel 2 mature protein.
PN   WO9603415-A1.
PD   08-FEB-1996.
PA   (HUMA-) HUMAN GENOME SCI INC.
       Query Match            6.4%;    Score 76.5;   DB 2;   Length 494;
       Best Local Similarity  21.3%;   Pred. No. 14;
RESULT 766
ID   AAW42996 standard; protein; 494 AA.
DE   Putative mature potassium channel 2 protein.
PN   US5710019-A.
PD   20-JAN-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
       Query Match            6.4%;    Score 76.5;   DB 2;   Length 494;
       Best Local Similarity  21.3%;   Pred. No. 14;
RESULT 767
ID   ABP58356 standard; protein; 494 AA.
DE   Human potassium channel subunit Kv5.1.
PN   WO200296944-A2.
PD   05-DEC-2002.
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
       Query Match            6.4%;    Score 76.5;   DB 6;   Length 494;
       Best Local Similarity  21.3%;   Pred. No. 14;
RESULT 768
ID   ADC99155 standard; protein; 494 AA.
DE   Human mature K+ channel 2 protein.
PN   US2003092895-A1.
PD   15-MAY-2003.
PA   (LIIY/) LI Y.
PA   (ADAM/) ADAMS M D.
PA   (WHIT/) WHITE O R.
       Query Match            6.4%;    Score 76.5;   DB 7;   Length 494;
       Best Local Similarity  21.3%;   Pred. No. 14;
RESULT 769
ID   AAW20085 standard; protein; 509 AA.
DE   Helicobacter pylori cytoplasmic protein, 10009666.aa.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR-) ASTRA AB.
       Query Match            6.4%;    Score 76.5;   DB 2;   Length 509;
       Best Local Similarity  19.2%;   Pred. No. 15;
RESULT 770
ID   ADQ07984 standard; protein; 526 AA.
DE   Human hypothetical protein FLJ20371-encoding cDNA.
PN   WO2004061123-A2.
PD   22-JUL-2004.
PA   (EXEL-) EXELIXIS INC.
       Query Match            6.4%;    Score 76.5;   DB 8;   Length 526;
       Best Local Similarity  15.7%;   Pred. No. 16;
RESULT 771
ID   ADP25065 standard; protein; 526 AA.
DE   PRO polypeptide SEQ ID NO:2243.
PN   WO2004041170-A2.
PD   21-MAY-2004.
PA   (GETH ) GENENTECH INC.
       Query Match            6.4%;    Score 76.5;   DB 8;   Length 526;
       Best Local Similarity  15.7%;   Pred. No. 16;
RESULT 772
ID   ADB63857 standard; protein; 555 AA.
DE   Human protein encoded by clone ASTR020053430.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
       Query Match            6.4%;    Score 76.5;   DB 7;   Length 555;
       Best Local Similarity  23.3%;   Pred. No. 17;
RESULT 773
ID   ABB08159 standard; protein; 570 AA.
DE   Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).
PN   WO200242330-A2.
PD   30-MAY-2002.
       Query Match            6.4%;
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PA   (INCY-) INCYTE GENOMICS INC.
      Query Match   6.4%;   Score 76.5;   DB 5;   Length 570;
      Best Local Similarity 23.3%;   Pred. No. 18;
RESULT 774
ID   AAW20918 standard; protein; 593 AA.
DE   H. pylori transporter protein, 14p12015orf14.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR) ASTRA AB.
RESULT 775
      Query Match   6.4%;   Score 76.5;   DB 2;   Length 593;
      Best Local Similarity 19.2%;   Pred. No. 19;
ID   ADN46225 standard; protein; 615 AA.
DE   Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
PN   WO2004022736-A1.
PD   18-MAR-2004.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
RESULT 776
      Query Match   6.4%;   Score 76.5;   DB 8;   Length 615;
      Best Local Similarity 22.6%;   Pred. No. 20;
ID   ADN21126 standard; protein; 2539 AA.
DB   Bacterial polypeptide #3779.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
      Query Match   6.4%;   Score 76.5;   DB 8;   Length 2539;
      Best Local Similarity 22.1%;   Pred. No. 1.4e+02;
RESULT 777
ID   ADH88107 standard; protein; 195 AA.
DE   Enterococcus faecalis polypeptide #2587.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
      Query Match   6.4%;   Score 76;   DB 7;   Length 195;
      Best Local Similarity 25.9%;   Pred. No. 4.6;
RESULT 778
ID   AAG09592 standard; protein; 274 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 779
      Query Match   6.4%;   Score 76;   DB 3;   Length 274;
      Best Local Similarity 26.7%;   Pred. No. 7.3;
ID   AAG09591 standard; protein; 287 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 7585.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 780
      Query Match   6.4%;   Score 76;   DB 3;   Length 287;
      Best Local Similarity 26.7%;   Pred. No. 7.8;
ID   ADQ96244 standard; protein; 366 AA.
DE   T cell activation associated protein #211.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
RESULT 781
      Query Match   6.4%;   Score 76;   DB 8;   Length 366;
      Best Local Similarity 22.0%;   Pred. No. 11;
ID   ADQ96246 standard; protein; 366 AA.
DE   T cell activation associated protein #212.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
RESULT 782
      Query Match   6.4%;   Score 76;   DB 8;   Length 366;
      Best Local Similarity 22.0%;   Pred. No. 11;
ID   ABB89424 standard; protein; 456 AA.
DE   Human polypeptide SEQ ID NO 1800.

PN   WO20019304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match   6.4%;   Score 76;   DB 5;   Length 456;
      Best Local Similarity 22.0%;   Pred. No. 15;
RESULT 783
ID   AAB53400 standard; protein; 557 AA.
DE   Human colon cancer antigen protein sequence SEQ ID NO:940.
PN   WO200055351-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match   6.4%;   Score 76;   DB 3;   Length 557;
      Best Local Similarity 22.0%;   Pred. No. 20;
RESULT 784
ID   AAY44945 standard; protein; 593 AA.
DE   Wheat sulphate permease-2.
PN   WO20004154-A2.
PD   27-JAN-2000.
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
      Query Match   6.4%;   Score 76;   DB 3;   Length 593;
      Best Local Similarity 21.4%;   Pred. No. 21;
RESULT 785
ID   ADN22849 standard; protein; 1402 AA.
DB   Bacterial polypeptide #5502.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
      Query Match   6.4%;   Score 76;   DB 8;   Length 1402;
      Best Local Similarity 20.2%;   Pred. No. 70;
RESULT 786
ID   ADN23383 standard; protein; 1917 AA.
DE   Bacterial polypeptide #6036.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
      Query Match   6.4%;   Score 76;   DB 8;   Length 1917;
      Best Local Similarity 18.5%;   Pred. No. 1.1e+02;
RESULT 787
ID   ABB61150 standard; protein; 228 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 16242.
PN   WO20017042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
      Query Match   6.3%;   Score 75.5;   DB 4;   Length 228;
      Best Local Similarity 21.8%;   Pred. No. 6.5;
RESULT 788
ID   ADK46633 standard; protein; 263 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 3148.
PN   US699703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
      Query Match   6.3%;   Score 75.5;   DB 8;   Length 263;
      Best Local Similarity 18.0%;   Pred. No. 7.9;
RESULT 789
ID   ADM92206 standard; protein; 263 AA.
DE   S pneumoniae antigenic protein sequence SeqID403.
PN   WO2004020609-A2.
PD   11-MAR-2004.
PA   (TUFT) UNIV TUFTS.
      Query Match   6.3%;   Score 75.5;   DB 8;   Length 263;
      Best Local Similarity 18.0%;   Pred. No. 7.9;
RESULT 790
ID   AAY81619 standard; protein; 264 AA.
DE   Streptococcus pneumoniae type 4 protein sequence #119.
PN   WO200006737-A2.

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PD   10-FEB-2000.
PA   (MICR-) MICROBIAL TECHNICS LTD.
     Query Match           6.3%;  Score 75.5;  DB 3;  Length 264;
     Best Local Similarity 18.0%;  Pred. No. 7.9;
RESULT 791
ID   ADR96242 standard; protein; 264 AA.
DE   Novel S. pneumoniae protein sequence, SEQ ID 4877.
PN   US6800744-B1.
PD   05-OCT-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match           6.3%;  Score 75.5;  DB 8;  Length 264;
     Best Local Similarity 18.0%;  Pred. No. 7.9;
RESULT 792
ID   ABU02182 standard; protein; 276 AA.
DE   S. pneumoniae type 4 strain protein from coding region #1759.
PN   WO200277021-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match           6.3%;  Score 75.5;  DB 6;  Length 276;
     Best Local Similarity 18.0%;  Pred. No. 8.4;
RESULT 793
ID   ABG93285 standard; protein; 342 AA.
DE   C. albicans BAX-associated protein fragment SEQ ID 528.
PN   WO200044906-A2.
PD   03-AUG-2000.
PA   (JANC ) JANSSEN PHARM NV.
     Query Match           6.3%;  Score 75.5;  DB 5;  Length 342;
     Best Local Similarity 21.9%;  Pred. No. 11;
RESULT 794
ID   AAB15936 standard; protein; 352 AA.
DE   E. coli proliferation associated protein sequence SEQ ID NO:293.
PN   WO200138533-A2.
PD   31-MAY-2001.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match           6.3%;  Score 75.5;  DB 3;  Length 352;
     Best Local Similarity 31.7%;  Pred. No. 12;
RESULT 795
ID   ADH51470 standard; protein; 363 AA.
DE   Rat MT1 receptor amino acid sequence #SEQ ID 2.
PN   FR2835847-A1.
PD   15-AUG-2003.
PA   (SERV-) LES LAB SERVIER SA.
     Query Match           6.3%;  Score 75.5;  DB 7;  Length 363;
     Best Local Similarity 23.5%;  Pred. No. 12;
RESULT 796
ID   AAU03851 standard; protein; 397 AA.
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #23.
PN   WO200138533-A2.
PD   31-MAY-2001.
PA   (PHAA ) PHARMACIA & UPJOHN.
     Query Match           6.3%;  Score 75.5;  DB 4;  Length 397;
     Best Local Similarity 19.1%;  Pred. No. 14;
RESULT 797
ID   AAU03852 standard; protein; 433 AA.
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #24.
PN   WO200138533-A2.
PD   31-MAY-2001.
PA   (PHAA ) PHARMACIA & UPJOHN.
     Query Match           6.3%;  Score 75.5;  DB 4;  Length 433;
     Best Local Similarity 19.1%;  Pred. No. 16;
RESULT 798
ID   ADS24239 standard; protein; 463 AA.
DE   Bacterial polypeptide #13272.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match           6.3%;  Score 75.5;  DB 8;  Length 463;
     Best Local Similarity 21.4%;  Pred. No. 17;

RESULT 799
ID   ADO29507 standard; protein; 471 AA.
DE   Mouse GPCR HTR2A, SEQ ID NO:609.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match           6.3%;  Score 75.5;  DB 8;  Length 471;
     Best Local Similarity 21.0%;  Pred. No. 18;
RESULT 800
ID   AAU03820 standard; protein; 499 AA.
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #19.
PN   WO200138533-A2.
PD   31-MAY-2001.
PA   (PHAA ) PHARMACIA & UPJOHN.
     Query Match           6.3%;  Score 75.5;  DB 4;  Length 499;
     Best Local Similarity 19.1%;  Pred. No. 19;
RESULT 801
ID   ADM72132 standard; protein; 392 AA.
DE   Human NTRAN polypeptide (clone ID 7524555CD1).
PN   WO2004022705-A2.
PD   18-MAR-2004.
PA   (INCY-) INCYTE CORP.
     Query Match           6.3%;  Score 75;  DB 8;  Length 392;
     Best Local Similarity 21.0%;  Pred. No. 16;
RESULT 802
ID   AAU45917 standard; protein; 445 AA.
DE   Propionibacterium acnes immunogenic protein #6813.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
     Query Match           6.3%;  Score 75;  DB 4;  Length 445;
     Best Local Similarity 24.8%;  Pred. No. 19;
RESULT 803
ID   ABM42436 standard; protein; 445 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
PN   WO200303515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
     Query Match           6.3%;  Score 75;  DB 6;  Length 445;
     Best Local Similarity 24.8%;  Pred. No. 19;
RESULT 804
ID   ADA34178 standard; protein; 467 AA.
DE   Acinetobacter baumannii protein #1339.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match           6.3%;  Score 75;  DB 6;  Length 467;
     Best Local Similarity 23.1%;  Pred. No. 20;
RESULT 805
ID   ADR14597 standard; protein; 473 AA.
DE   Human NF-kappaB pathway-associated protein SeqID598.
PN   WO2004065577-A2.
PD   05-AUG-2004.
PA   (BRIM/) BRISTOL-MYERS SQUIBB CO.
     Query Match           6.3%;  Score 75;  DB 8;  Length 473;
     Best Local Similarity 21.0%;  Pred. No. 20;
RESULT 806
ID   ADP99138 standard; protein; 480 AA.
DE   Human transporter and ion channel (TRICH) protein - SEQ ID 3.
PN   WO2004048599-A2.
PD   10-JUN-2004.
PA   (INCY-) INCYTE CORP.
     Query Match           6.3%;  Score 75;  DB 8;  Length 480;
     Best Local Similarity 21.0%;  Pred. No. 21;
RESULT 807
ID   ADH86490 standard; protein; 549 AA.
DE   Enterococcus faecalis polypeptide #970.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match           6.3%;  Score 75;  DB 7;  Length 549;
     Best Local Similarity 18.7%;  Pred. No. 25;
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RESULT 808
ID AAR54066 standard; protein; 1051 AA.
DE Non-A, non-B hepatitis virus gene #4 product.
PN JP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU) TONEN CORP.
    Query Match   6.3%; Score 75; DB 2; Length 1051;
    Best Local Similarity 23.4%; Pred. No. 62;

RESULT 809
ID AAR98361 standard; protein; 1051 AA.
DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
PN JP07133291-A.
PD 23-MAY-1995.
PA (TOFU) TONEN CORP.
    Query Match   6.3%; Score 75; DB 2; Length 1051;
    Best Local Similarity 23.4%; Pred. No. 62;

RESULT 810
ID ADB64712 standard; protein; 1131 AA.
DE Human protein encoded by clone NT2NE20077270.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
    Query Match   6.3%; Score 75; DB 7; Length 1131;
    Best Local Similarity 23.9%; Pred. No. 68;

RESULT 811
ID AAB64494 standard; protein; 2248 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20274.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   6.3%; Score 75; DB 8; Length 2248;
    Best Local Similarity 22.9%; Pred. No. 1.8e+02;

RESULT 812
ID ADG20763 standard; protein; 2248 AA.
DE Drosophila melanogaster rutabaga protein SEQ ID NO:2.
PN WO2003103704-A2.
PD 18-DEC-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
    Query Match   6.3%; Score 75; DB 8; Length 2248;
    Best Local Similarity 22.9%; Pred. No. 1.8e+02;

RESULT 813
ID ADQ89656 standard; protein; 2248 AA.
DE Antagonist of cell cycle progression polypeptide #43.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
    Query Match   6.3%; Score 75; DB 8; Length 2248;
    Best Local Similarity 22.9%; Pred. No. 1.8e+02;

RESULT 814
ID AAB66797 standard; protein; 200 AA.
DE Rat 164-1h protein (SeqID 13).
PN WO200102858-A1.
PD 11-JAN-2001.
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA (MATE-) INST MATERIALS RES & ENG.
    Query Match   6.2%; Score 74.5; DB 4; Length 200;
    Best Local Similarity 23.8%; Pred. No. 7.1;

RESULT 815
ID ADP74954 standard; protein; 256 AA.
DE Porcine reproductive and respiratory syndrome virus ORF #5 protein.
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
    Query Match   6.2%; Score 74.5; DB 8; Length 256;
    Best Local Similarity 23.3%; Pred. No. 10;

RESULT 816
ID AAR53748 standard; protein; 355 AA.
DE Seven transmembrane receptor (V28).
PN WO9412635-A2.
PD 09-JUN-1994.

PA (ICOS-) ICOS CORP.
    Query Match   6.2%; Score 74.5; DB 2; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 817
ID AAW48722 standard; protein; 355 AA.
DE Human V28 seven transmembrane receptor.
PN US5759804-A.
PD 02-JUN-1998.
PA (ICOS-) ICOS CORP.
    Query Match   6.2%; Score 74.5; DB 2; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 818
ID AAY90677 standard; protein; 355 AA.
DE Human mutant G protein-coupled receptor V28 (I230K).
PN WO20022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
    Query Match   6.2%; Score 74.5; DB 3; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 819
ID AAY90642 standard; protein; 355 AA.
DE Human G protein-coupled receptor V28.
PN WO20022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
    Query Match   6.2%; Score 74.5; DB 3; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 820
ID AAB21693 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #2.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
    Query Match   6.2%; Score 74.5; DB 3; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 821
ID AAB21692 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #1.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
    Query Match   6.2%; Score 74.5; DB 3; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 822
ID AAG80126 standard; protein; 355 AA.
DE Human CX3CR1 protein.
PN WO200172830-A2.
PD 04-OCT-2001.
PA (IPFP-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
    Query Match   6.2%; Score 74.5; DB 4; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 823
ID AAB82786 standard; protein; 355 AA.
DE Human CX3C chemokine receptor 1.
PN WO200160406-A1.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PHARM INC.
PA (NOUN) UNIV NORTHWESTERN.
    Query Match   6.2%; Score 74.5; DB 4; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 824
ID AAU91235 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #2.
PN US6348574-B1.
PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
    Query Match   6.2%; Score 74.5; DB 5; Length 355;
    Best Local Similarity 25.8%; Pred. No. 16;

RESULT 825
ID AAU91234 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #1.
PN US6348574-B1.

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PD   19-FEB-2002.
PA   (ICOS-) ICOS CORP.
     Query Match             6.2%;   Score 74.5;  DB 5;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 826
ID   AAU84327 standard; protein; 355 AA.
DE   Protein CX3CR1 differentially expressed in breast cancer tissue.
PN   WO200210436-A2.
PD   07-FEB-2002.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
PA   (BAAK/) BAAK J.
     Query Match             6.2%;   Score 74.5;  DB 5;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 827
ID   ABR58524 standard; protein; 355 AA.
DE   Human chemokine (C-X3-C) receptor 1 protein.
PN   WO200325138-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match             6.2%;   Score 74.5;  DB 6;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 828
ID   AAO29513 standard; protein; 355 AA.
DE   Human fractalkine receptor (313) protein.
PN   WO200039475-A2.
PD   15-MAY-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match             6.2%;   Score 74.5;  DB 6;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 829
ID   ABP97732 standard; protein; 355 AA.
DE   Amino acid sequence of human chemokine receptor CX3CR1.
PN   WO200314153-A2.
PD   20-FEB-2003.
PA   (TOPI-) TOPIGEN PHARM INC.
     Query Match             6.2%;   Score 74.5;  DB 6;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 830
ID   ABP81882 standard; protein; 355 AA.
DE   Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match             6.2%;   Score 74.5;  DB 6;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 831
ID   ADC22751 standard; protein; 355 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #74.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match             6.2%;   Score 74.5;  DB 7;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 832
ID   ADC22649 standard; protein; 355 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #34.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match             6.2%;   Score 74.5;  DB 7;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 833
ID   ADH14224 standard; protein; 355 AA.
DE   Mutated human serotonin V28.
PN   US200310529-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BBHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match             6.2%;   Score 74.5;  DB 7;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 834
ID   ADH14122 standard; protein; 355 AA.
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DE   Human serotonin V28.
PN   US200310529-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match             6.2%;   Score 74.5;  DB 7;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 835
ID   ADH10680 standard; protein; 355 AA.
DE   Human CX3CR1 polypeptide.
PN   WO200310484-A1.
PD   18-DEC-2003.
PA   (META-) METABOLEX INC.
     Query Match             6.2%;   Score 74.5;  DB 8;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 836
ID   ADO29269 standard; protein; 355 AA.
DE   Human GPCR CX3CR1, SEQ ID NO:370.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match             6.2%;   Score 74.5;  DB 8;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 837
ID   ADQ18141 standard; protein; 355 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 958.
PN   WO200448938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match             6.2%;   Score 74.5;  DB 8;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 838
ID   ADP56020 standard; protein; 355 AA.
DE   Human PRO protein sequence SEQ ID NO:1996.
PN   WO200403956-A2.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             6.2%;   Score 74.5;  DB 8;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 839
ID   ADP54585 standard; protein; 355 AA.
DE   Human PRO protein sequence SEQ ID NO:561.
PN   WO200403956-A2.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             6.2%;   Score 74.5;  DB 8;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 840
ID   ADP23931 standard; protein; 355 AA.
DE   PRO polypeptide SEQ ID NO:1109.
PN   WO200404170-A2.
PD   21-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             6.2%;   Score 74.5;  DB 8;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 841
ID   ADQ39421 standard; protein; 355 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1084.
PN   WO200405052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match             6.2%;   Score 74.5;  DB 8;  Length 355;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 842
ID   ADQ39422 standard; protein; 362 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1085.
PN   WO200405052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match             6.2%;   Score 74.5;  DB 8;  Length 362;
     Best Local Similarity  25.8%;   Pred. No. 16;
RESULT 843
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ID  AAW77109 standard; protein; 471 AA.
DE  Rat 5-HT2A serotonin receptor C322K mutant.
PN  WO9838217-A1.
PD  03-SEP-1998.
PA  (TEIT/) TEITLER M.
PA  (HERR/) HERRICK-DAVIS K.
PA  (EGAN/) EGAN C C.
    Query Match         6.2%;   Score 74.5;  DB 2;  Length 471;
    Best Local Similarity  21.0%;  Pred. No. 23;
RESULT 844
ID  AAW77111 standard; protein; 471 AA.
DE  Rat 5-HT2A serotonin receptor C322E mutant.
PN  WO9838217-A1.
PD  03-SEP-1998.
PA  (TEIT/) TEITLER M.
PA  (HERR/) HERRICK-DAVIS K.
PA  (EGAN/) EGAN C C.
    Query Match         6.2%;   Score 74.5;  DB 2;  Length 471;
    Best Local Similarity  21.0%;  Pred. No. 23;
RESULT 845
ID  AAW77110 standard; protein; 471 AA.
DE  Rat 5-HT2A serotonin receptor C322R mutant.
PN  WO9838217-A1.
PD  03-SEP-1998.
PA  (TEIT/) TEITLER M.
PA  (HERR/) HERRICK-DAVIS K.
PA  (EGAN/) EGAN C C.
    Query Match         6.2%;   Score 74.5;  DB 2;  Length 471;
    Best Local Similarity  21.0%;  Pred. No. 23;
RESULT 846
ID  AAW77104 standard; protein; 471 AA.
DE  Rat 5-HT2A serotonin receptor.
PN  WO9838217-A1.
PD  03-SEP-1998.
PA  (TEIT/) TEITLER M.
PA  (HERR/) HERRICK-DAVIS K.
PA  (EGAN/) EGAN C C.
    Query Match         6.2%;   Score 74.5;  DB 2;  Length 471;
    Best Local Similarity  21.0%;  Pred. No. 23;
RESULT 847
ID  ABB07980 standard; protein; 471 AA.
DE  Rat 5-HT2 receptor sequence.
PN  US5383762-B1.
PD  07-MAY-2002.
PA  (SYNA-) SYNAPTIC PHARM CORP.
    Query Match         6.2%;   Score 74.5;  DB 5;  Length 471;
    Best Local Similarity  21.0%;  Pred. No. 23;
RESULT 848
ID  ADF74971 standard; protein; 481 AA.
DE  Rat 164-1b protein (SeqID 30).
PN  WO2003097686-A1.
PD  27-NOV-2003.
PA  (HELI-) HELIX RES INST.
    Query Match         6.2%;   Score 74.5;  DB 4;  Length 481;
    Best Local Similarity  23.3%;  Pred. No. 24;
RESULT 849
ID  AAM93692 standard; protein; 562 AA.
DE  Human polypeptide, SEQ ID NO: 3602.
PN  EP1130094-A2.
PD  05-SEP-2001.
PA  (HELI-) HELIX RES INST.
    Query Match         6.2%;   Score 74.5;  DB 5;  Length 562;
    Best Local Similarity  21.0%;  Pred. No. 23;
RESULT 850
ID  ADL31569 standard; protein; 562 AA.
DE  Human protein encoded by a full length cDNA clone SeqID 3602.
PN  EP1396543-A2.
PD  10-MAR-2004.
PA  (REAS-) RES ASSOC BIOTECHNOLOGY.
    Query Match         6.2%;   Score 74.5;  DB 8;  Length 562;
    Best Local Similarity  23.1%;  Pred. No. 30;
RESULT 851
ID  ADQ96138 standard; protein; 562 AA.
DE  T cell activation associated protein #158.
PN  WO2004058805-A2.
PD  15-JUL-2004.
PA  (ASAH-) ASAHI KASEI PHARMA CORP.
    Query Match         6.2%;   Score 74.5;  DB 8;  Length 562;
    Best Local Similarity  23.1%;  Pred. No. 30;
RESULT 852
ID  ADR86160 standard; protein; 587 AA.
DE  Aspergillus fumigatus essential gene protein #210.
PN  WO2004067709-A2.
PD  12-AUG-2004.
PA  (ELIT-) ELITRA PHARM INC.
PA  (ELIT-) ELITRA CANADA LTD.
    Query Match         6.2%;   Score 74.5;  DB 8;  Length 587;
    Best Local Similarity  18.2%;  Pred. No. 32;
RESULT 853
ID  ABB62948 standard; protein; 597 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 15636.
PN  WO20071042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
    Query Match         6.2%;   Score 74.5;  DB 4;  Length 597;
    Best Local Similarity  27.2%;  Pred. No. 32;
RESULT 854
ID  ADA36878 standard; protein; 940 AA.
DE  Acinetobacter baumannii protein #4039.
PN  US6562958-B1.
PD  13-MAY-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match         6.2%;   Score 74.5;  DB 6;  Length 940;
    Best Local Similarity  21.1%;  Pred. No. 61;
RESULT 855
ID  ABB92731 standard; protein; 1808 AA.
DE  Herbicidally active polypeptide SEQ ID NO 1942.
PN  WO20021010-A2.
PD  07-FEB-2002.
PA  (FARB ) BAYER AG.
    Query Match         6.2%;   Score 74.5;  DB 5;  Length 1808;
    Best Local Similarity  17.3%;  Pred. No. 1.5e+02;
RESULT 856
ID  AAE20477 standard; protein; 3010 AA.
DE  HCV-S1 full-length polyprotein.
PN  WO20020447-A2.
PD  31-JAN-2002.
PA  (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA  (EHRL/) EHRLICH G.
    Query Match         6.2%;   Score 74.5;  DB 5;  Length 3010;
    Best Local Similarity  23.8%;  Pred. No. 3e+02;
RESULT 857
ID  ADF07294 standard; protein; 154 AA.
DE  Bacterial polypeptide #3407.
PN  US6605709-B1.
PD  12-AUG-2003.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match         6.2%;   Score 74;  DB 7;  Length 154;
    Best Local Similarity  26.4%;  Pred. No. 5.6;
RESULT 858
ID  ABU70365 standard; protein; 231 AA.
DE  Human adipocyte bait protein, melatonin receptor_V4.
PN  WO200286122-A2.
PD  31-OCT-2002.
PA  (HYBR-) HYBRIGENICS.
    Query Match         6.2%;   Score 74;  DB 6;  Length 231;
    Best Local Similarity  18.5%;  Pred. No. 9.9;
RESULT 859
ID  ABU70366 standard; protein; 231 AA.
DE  Human adipocyte bait protein, melatonin receptor_V5_
PN  WO200286122-A2.
PD  31-OCT-2002.
PA  (HYBR-) HYBRIGENICS.
    Query Match         6.2%;   Score 74;  DB 6;  Length 231;
    Best Local Similarity  18.5%;  Pred. No. 9.9;
RESULT 860
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ID    ABB54180 standard; protein; 312 AA.
DE    Lactococcus lactis protein yiIG.
PN    FR2807446-A1.
PD    12-OCT-2001.
PA    (INRG ) INRA INST NAT RECH AGRONOMIQUE.
      Query Match          6.2%;   Score 74;   DB 5;   Length 312;
      Best Local Similarity  24.3%;   Pred. No. 15;
RESULT 861
ID    ADS44483 standard; protein; 312 AA.
DE    Bacterial polypeptide #22913.
PN    US2003233675-A1.
PD    18-DEC-2003.
PA    (CAOY/) CAO Y.
PA    (HINK/) HINKLE G J.
PA    (SLAT/) SLATER S C.
PA    (CHEN/) CHEN X.
PA    (GOLD/) GOLDMAN B S.
      Query Match          6.2%;   Score 74;   DB 8;   Length 312;
      Best Local Similarity  24.3%;   Pred. No. 15;
RESULT 862
ID    ABU02869 standard; protein; 324 AA.
DE    S. pneumoniae type 4 strain protein from coding region #2450.
PN    WO200277021-A2.
PD    03-OCT-2002.
PA    (CHIR-) CHIRON SPA.
      Query Match          6.2%;   Score 74;   DB 6;   Length 324;
      Best Local Similarity  24.3%;   Pred. No. 16;
RESULT 863
ID    ADR94027 standard; protein; 332 AA.
DE    Novel S. pneumoniae protein sequence, SEQ ID 2662.
PN    US6800744-B1.
PD    05-OCT-2004.
PA    (GENO-) INST GENOMIC RES.
      Query Match          6.2%;   Score 74;   DB 8;   Length 332;
      Best Local Similarity  24.3%;   Pred. No. 16;
RESULT 864
ID    ABO00448 standard; protein; 342 AA.
DE    Novel human polypeptide #35.
PN    WO2003023013-A2.
PD    20-MAR-2003.
PA    (HYSE-) HYSEQ INC.
      Query Match          6.2%;   Score 74;   DB 6;   Length 342;
      Best Local Similarity  21.2%;   Pred. No. 17;
RESULT 865
ID    AAR88412 standard; protein; 350 AA.
DE    High-affinity melatonin-1a receptor.
PN    WO9535320-A1.
PD    28-DEC-1995.
PA    (MASS-) MASSACHUSETTS GEN HOSPITAL.
      Query Match          6.2%;   Score 74;   DB 2;   Length 350;
      Best Local Similarity  18.5%;   Pred. No. 18;
RESULT 866
ID    AAW15786 standard; protein; 350 AA.
DE    Melatonin receptor protein.
PN    JP09084581-A.
PD    31-MAR-1997.
PA    (TAKE ) TAKEDA CHEM IND LTD.
      Query Match          6.2%;   Score 74;   DB 2;   Length 350;
      Best Local Similarity  18.5%;   Pred. No. 18;
RESULT 867
ID    AAW94761 standard; protein; 350 AA.
DE    Human melatonin receptor protein mel-1a.
PN    EP892046-A2.
PD    20-JAN-1999.
PA    (JCRP-) JCR PHARM CO LTD.
      Query Match          6.2%;   Score 74;   DB 2;   Length 350;
      Best Local Similarity  18.5%;   Pred. No. 18;
RESULT 868
ID    ABP81840 standard; protein; 350 AA.
DE    Human melatonin receptor type 1a protein SEQ ID NO:164.
PN    WO200261087-A2.
PD    08-AUG-2002.

PA    (LIFE-) LIFESPAN BIOSCIENCES INC.
      Query Match          6.2%;   Score 74;   DB 6;   Length 350;
      Best Local Similarity  18.5%;   Pred. No. 18;
RESULT 869
ID    ADO29552 standard; protein; 350 AA.
DE    Human GPCR MTNR1A, SEQ ID NO:654.
PN    WO2004040000-A2.
PD    13-MAY-2004.
PA    (PRIM-) PRIMAL INC.
      Query Match          6.2%;   Score 74;   DB 8;   Length 350;
      Best Local Similarity  18.5%;   Pred. No. 18;
RESULT 870
ID    AAW19220 standard; protein; 364 AA.
DE    Rat growth hormone secretagogue receptor type Ia.
PN    WO9721730-A1.
PD    19-JUN-1997.
PA    (MERI ) MERCK & CO INC.
      Query Match          6.2%;   Score 74;   DB 2;   Length 364;
      Best Local Similarity  19.4%;   Pred. No. 19;
RESULT 871
ID    ABM73179 standard; protein; 366 AA.
DE    Staphylococcus aureus protein #2419.
PN    WO200294868-A2.
PD    28-NOV-2002.
PA    (CHIR-) CHIRON SPA.
      Query Match          6.2%;   Score 74;   DB 6;   Length 366;
      Best Local Similarity  21.8%;   Pred. No. 19;
RESULT 872
ID    ABB55224 standard; protein; 442 AA.
DE    Lactococcus lactis protein yteD.
PN    FR2807446-A1.
PD    12-OCT-2001.
PA    (INRG ) INRA INST NAT RECH AGRONOMIQUE.
      Query Match          6.2%;   Score 74;   DB 5;   Length 442;
      Best Local Similarity  20.4%;   Pred. No. 24;
RESULT 873
ID    ADN23927 standard; protein; 485 AA.
DE    Bacterial polypeptide #6580.
PN    US2003233675-A1.
PD    18-DEC-2003.
PA    (CAOY/) CAO Y.
PA    (HINK/) HINKLE G J.
PA    (SLAT/) SLATER S C.
PA    (CHEN/) CHEN X.
PA    (GOLD/) GOLDMAN B S.
      Query Match          6.2%;   Score 74;   DB 8;   Length 485;
      Best Local Similarity  26.2%;   Pred. No. 28;
RESULT 874
ID    AAY80509 standard; protein; 492 AA.
DE    F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
PN    WO200008170-A1.
PD    17-FEB-2000.
PA    (SAOC ) MERCIAN CORP.
      Query Match          6.2%;   Score 74;   DB 3;   Length 492;
      Best Local Similarity  22.5%;   Pred. No. 28;
RESULT 875
ID    AAG64105 standard; protein; 493 AA.
DE    Flavobacterium lutescens L-lysine-6-aminotransferase.
PN    WO20014216-A1.
PD    05-JUL-2001.
PA    (SAOC ) MERCIAN CORP.
      Query Match          6.2%;   Score 74;   DB 4;   Length 493;
      Best Local Similarity  22.5%;   Pred. No. 28;
RESULT 876
ID    AAR54067 standard; protein; 1031 AA.
DE    Non-A, non-B hepatitis virus gene #6 product.
PN    JP06141870-A.
PD    24-MAY-1994.
PA    (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA    (SANW ) SANWA KAGAKU KENKYUSHO CO.
PA    (TOFU ) TONEN CORP.
      Query Match          6.2%;   Score 74;   DB 2;   Length 1031;
      Best Local Similarity  26.2%;   Pred. No. 79;
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RESULT 877
ID   AAR98362 standard; protein; 1031 AA.
DE   5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).
PN   JP07133291-A.
PD   23-MAY-1995.
PA   (TOFU) TONEN CORP.
     Query Match   6.2%; Score 74; DB 2; Length 1031;
     Best Local Similarity   26.2%; Pred. No. 79;
RESULT 878
ID   AAG59839 standard; protein; 120 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
PN   EP103340S-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 120;
     Best Local Similarity   20.3%; Pred. No. 4.6;
RESULT 879
ID   AAU25578 standard; protein; 192 AA.
DE   Human G Protein-Coupled Receptor (GPCR) polypeptide #25.
PN   WO200162797-A2.
PD   30-AUG-2001.
PA   (PHAA) PHARMACIA & UPJOHN CO.
     Query Match   6.2%; Score 73.5; DB 4; Length 192;
     Best Local Similarity   26.3%; Pred. No. 8.8;
RESULT 880
ID   ABU44044 standard; protein; 268 AA.
DE   Protein encoded by Prokaryotic essential gene #29571.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.2%; Score 73.5; DB 6; Length 268;
     Best Local Similarity   19.6%; Pred. No. 14;
RESULT 881
ID   AAG32488 standard; protein; 282 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
PN   EP103340S-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 282;
     Best Local Similarity   28.1%; Pred. No. 15;
RESULT 882
ID   ADF05982 standard; protein; 312 AA.
DE   Bacterial polypeptide #2095.
PN   US660S709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   6.2%; Score 73.5; DB 7; Length 312;
     Best Local Similarity   17.4%; Pred. No. 17;
RESULT 883
ID   AAG51386 standard; protein; 377 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN   EP103340S-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 377;
     Best Local Similarity   28.1%; Pred. No. 22;
RESULT 884
ID   AAG32487 standard; protein; 377 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN   EP103340S-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 377;
     Best Local Similarity   28.1%; Pred. No. 22;
RESULT 885
ID   ADQ75734 standard; protein; 404 AA.
DE   Codon optimised hCMV IE1 encoded exons 2 and 4.
PN   WO200405166-A2.
PD   15-JUL-2004.
PA   (VICA-) VICAL INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 404;
     Best Local Similarity   19.3%; Pred. No. 25;
RESULT 886
ID   AAG51385 standard; protein; 442 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN   EP103340S-A2.
PD   06-SEP-2000.

     Query Match   6.2%; Score 73.5; DB 3; Length 442;
     Best Local Similarity   28.1%; Pred. No. 28;
RESULT 887
ID   AAG32486 standard; protein; 442 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN   EP103340S-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 442;
     Best Local Similarity   28.1%; Pred. No. 28;
RESULT 888
ID   AAG51384 standard; protein; 489 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN   EP103340S-A2.
PD   06-SEP-2000.
     Query Match   6.2%; Score 73.5; DB 3; Length 489;
     Best Local Similarity   28.1%; Pred. No. 32;
RESULT 889
ID   AAB86544 standard; protein; 491 AA.
DE   Human cytomegalovirus strain AD169 IE1 protein.
PN   WO200163286-A2.
PD   30-AUG-2001.
PA   (KERN/) KERN F.
     Query Match   6.2%; Score 73.5; DB 4; Length 491;
     Best Local Similarity   19.3%; Pred. No. 32;
RESULT 890
ID   ADP12517 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #127.
PN   WO200404234S-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 32;
RESULT 891
ID   ADP12518 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #128.
PN   WO200404234S-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 32;
RESULT 892
ID   ADP12513 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #123.
PN   WO200404234S-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 32;
RESULT 893
ID   ADP12514 standard; protein; 491 AA.
DE   Protein encoded by mRNA of the invention #124.
PN   WO200404234S-A2.
PD   21-MAY-2004.
PA   (EXPR-) EXPRESSION DIAGNOSTICS INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 32;
RESULT 894
ID   ADQ75725 standard; protein; 491 AA.
DE   Wild type hCMV IE1.
PN   WO200405166-A2.
PD   15-JUL-2004.
PA   (VICA-) VICAL INC.
     Query Match   6.2%; Score 73.5; DB 8; Length 491;
     Best Local Similarity   19.3%; Pred. No. 32;
RESULT 895
ID   ABP73574 standard; protein; 574 AA.
DE   Candida albicans essential protein SEQ ID NO 7411.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.2%; Score 73.5; DB 5; Length 574;
     Best Local Similarity   20.8%; Pred. No. 40;
RESULT 896

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ID   ADS28278 standard; protein; 637 AA.
DE   Bacterial polypeptide #17311.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
  Query Match             6.2%;  Score 73.5; DB 8;  Length 637
  Best Local Similarity   28.3%;  Pred. No. 46;
RESULT 897
ID   ABG29128 standard; protein; 682 AA.
DE   Novel human diagnostic protein #29119.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             6.2%;  Score 73.5; DB 4;  Length 682;
  Best Local Similarity   20.0%;  Pred. No. 51;
RESULT 898
ID   ABB61737 standard; protein; 1287 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 12003.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
  Query Match             6.2%;  Score 73.5; DB 4;  Length 1287;
  Best Local Similarity   18.2%;  Pred. No. 1.2e+02;
RESULT 899
ID   ADS96670 standard; protein; 1287 AA.
DE   Drosophila melanogaster protein, SEQ ID 291.
PN   WO2004039999-A2.
PD   13-MAY-2004.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match             6.2%;  Score 73.5; DB 8;  Length 1287;
  Best Local Similarity   18.2%;  Pred. No. 1.2e+02;
RESULT 900
ID   AAR33214 standard; protein; 3033 AA.
DE   NANBH virus strain HC-J8 protein.
PN   EP532167-A2.
PD   17-MAR-1993.
PA   (IMMO ) IMMUNO JAPAN INC.
  Query Match             6.2%;  Score 73.5; DB 2;  Length 3033;
  Best Local Similarity   27.4%;  Pred. No. 4e+02;
RESULT 901
ID   AAW20571 standard; protein; 114 AA.
DE   H. pylori secreted or periplasmic protein 80257.aa.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (PHAA ) PHARMACIA & UPJOHN CO.
  Query Match             6.1%;  Score 73; DB 5;  Length 114;
  Best Local Similarity   20.3%;  Pred. No. 9.8;
RESULT 902
ID   ADC97146 standard; protein; 199 AA.
DE   E. faecium protein sequence SEQ ID 6773.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             6.1%;  Score 73; DB 7;  Length 199;
  Best Local Similarity   22.6%;  Pred. No. 11;
RESULT 904
ID   ABP29367 standard; protein; 249 AA.
DE   Streptococcus polypeptide SEQ ID NO 7910.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
  Query Match             6.1%;  Score 73; DB 5;  Length 249;
  Best Local Similarity   24.6%;  Pred. No. 14;
RESULT 905
ID   AAU87836 standard; protein; 272 AA.
DE   T. aureum 7091 elongase TELO1 from plasmid pRAT-4-A1.
PN   WO200208401-A2.
PD   31-JAN-2002.
PA   (ABBO ) ABBOTT LAB.
  Query Match             6.1%;  Score 73; DB 5;  Length 272;
  Best Local Similarity   19.9%;  Pred. No. 16;
RESULT 906
ID   ADH80191 standard; protein; 272 AA.
DE   Fungal 7091 elongase protein seq id 75.
PN   US203163845-A1.
PD   28-AUG-2003.
PA   (MUKE/) MUKERJI P.
PA   (LEON/) EUN-YEONG LEONARD A.
PA   (HUAN/) HUANG Y.
PA   (PERE/) PEREIRA S L.
  Query Match             6.1%;  Score 73; DB 8;  Length 272;
  Best Local Similarity   19.9%;  Pred. No. 16;
RESULT 907
ID   ABM73154 standard; protein; 290 AA.
DE   Staphylococcus aureus protein #2394.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
  Query Match             6.1%;  Score 73; DB 6;  Length 290;
  Best Local Similarity   23.4%;  Pred. No. 18;
RESULT 908
ID   ABR47464 standard; protein; 322 AA.
DE   Breast cancer associated protein sequence SEQ ID NO:160.
PN   WO200300989-A2.
PD   16-JAN-2003.
PA   (MILL-) MILLENIUM PHARM INC.
  Query Match             6.1%;  Score 73; DB 6;  Length 322;
  Best Local Similarity   20.6%;  Pred. No. 21;
RESULT 909
ID   ADN61865 standard; protein; 349 AA.
DE   Human novel protein NOV42a.
PN   US200404382-A1.
PD   04-MAR-2004.
PA   (PADI/) PADIGARU M.
PA   (SPYT/) SPYTEK K A.
PA   (SHEN/) SHENOY S G.
PA   (TAUP/) TAUPIER R J.
PA   (PENA/) PENA C E A.
PA   (LILL/) LI L.
PA   (ZERH/) ZERHUSEN B D.
PA   (GUSE/) GUSEV V Y.
PA   (JIWW/) JI W.
PA   (GORM/) GORMAN L.
PA   (MILL/) MILLER C E.
PA   (KEKU/) KEKUDA R.
PA   (PATT/) PATTURAJAN M.
PA   (GANG/) GANGOLLI E A.
PA   (VERN/) VERNET C A M.
PA   (GUOX/) GUO X S.
PA   (TCHE/) TCHERNEV V T.
PA   (FERN/) FERNANDES E R.
PA   (CASM/) CASMAN S J.
PA   (MALY/) MALYANKAR U M.
PA   (GERL/) GERLACH V.
PA   (LIUY/) LIU Y.
PA   (ANDE/) ANDERSON D W.
PA   (SPAD/) SPADERNA S K.
PA   (CATT/) CATTERTON E.
PA   (LEIT/) LEITE M W.
PA   (ZHON/) ZHONG H.
PA   (ALSO/) ALSOBROOK J P.
PA   (LEPL/) LEPLEY D M.
PA   (RIEG/) RIEGER D K.
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PA   (BURG/) BURGESS C E.
    Query Match   6.1%;   Score 73;   DB 8;   Length 349;
    Best Local Similarity   24.0%;   Pred. No. 23;
RESULT 910
ID   AAW19613 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor type Ia.
PN   WO972204-A1.
PD   19-JUN-1997.
PA   (MERI) MERCK & CO INC.
    Query Match   6.1%;   Score 73;   DB 2;   Length 364;
    Best Local Similarity   19.4%;   Pred. No. 24;
RESULT 911
ID   AAY54565 standard; protein; 364 AA.
DE   A mouse growth hormone secretagogue receptor.
PN   WO200004000-A2.
PD   20-JAN-2000.
PA   (MERI) MERCK & CO INC.
    Query Match   6.1%;   Score 73;   DB 3;   Length 364;
    Best Local Similarity   19.4%;   Pred. No. 24;
RESULT 912
ID   AAB97377 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor (GHSR) related protein.
PN   WO200132705-A1.
PD   10-MAY-2001.
PA   (TAKE) TAKEDA CHEM IND LTD.
    Query Match   6.1%;   Score 73;   DB 4;   Length 364;
    Best Local Similarity   19.4%;   Pred. No. 24;
RESULT 913
ID   ADO29026 standard; protein; 364 AA.
DE   Mouse novel GPCR GHSR, SEQ ID NO:125.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
    Query Match   6.1%;   Score 73;   DB 8;   Length 364;
    Best Local Similarity   19.4%;   Pred. No. 24;
RESULT 914
ID   AAW77773 standard; protein; 377 AA.
DE   Staphylococcus aureus protein of unknown function.
PN   EP841394-A2.
PD   13-MAY-1998.
PA   (SMIK) SMITHKLINE BEECHAM CORP.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
    Query Match   6.1%;   Score 73;   DB 2;   Length 377;
    Best Local Similarity   23.3%;   Pred. No. 26;
RESULT 915
ID   AAG50065 standard; protein; 415 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
PN   EP1033405-A2.
PD   06-SEP-2000.
    Query Match   6.1%;   Score 73;   DB 3;   Length 415;
    Best Local Similarity   19.8%;   Pred. No. 29;
RESULT 916
ID   AAG24013 standard; protein; 427 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 27528.
PN   EP1033405-A2.
PD   06-SEP-2000.
    Query Match   6.1%;   Score 73;   DB 3;   Length 427;
    Best Local Similarity   22.0%;   Pred. No. 30;
RESULT 917
ID   AAG24012 standard; protein; 430 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
PN   EP1033405-A2.
PD   06-SEP-2000.
    Query Match   6.1%;   Score 73;   DB 3;   Length 430;
    Best Local Similarity   22.0%;   Pred. No. 31;
RESULT 918
ID   ABU31419 standard; protein; 453 AA.
DE   Protein encoded by Prokaryotic essential gene #16946.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
    Query Match   6.1%;   Score 73;   DB 6;   Length 453;
    Best Local Similarity   26.5%;   Pred. No. 33;

RESULT 919
ID   AAG50064 standard; protein; 472 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
PN   EP1033405-A2.
PD   06-SEP-2000.
    Query Match   6.1%;   Score 73;   DB 3;   Length 472;
    Best Local Similarity   19.8%;   Pred. No. 35;
RESULT 920
ID   AAG50063 standard; protein; 474 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63402.
PN   EP1033405-A2.
PD   06-SEP-2000.
    Query Match   6.1%;   Score 73;   DB 3;   Length 474;
    Best Local Similarity   19.8%;   Pred. No. 35;
RESULT 921
ID   ABM70313 standard; protein; 490 AA.
DE   Photorhabdus luminescens protein sequence #3410.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
    Query Match   6.1%;   Score 73;   DB 6;   Length 490;
    Best Local Similarity   24.6%;   Pred. No. 37;
RESULT 922
ID   AAY33766 standard; protein; 495 AA.
DE   hKv5.1 human brain-specific potassium channel.
PN   WO941372-A1.
PD   19-AUG-1999.
PA   (ZENE) ZENECA LTD.
    Query Match   6.1%;   Score 73;   DB 2;   Length 495;
    Best Local Similarity   23.2%;   Pred. No. 37;
RESULT 923
ID   ABO63300 standard; protein; 501 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9817.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   6.1%;   Score 73;   DB 7;   Length 501;
    Best Local Similarity   26.5%;   Pred. No. 38;
RESULT 924
ID   ABP53583 standard; protein; 526 AA.
DE   Human NOV13b protein SEQ ID NO:30.
PN   WO200262999-A2.
PD   15-AUG-2002.
PA   (CURA-) CURAGEN CORP.
    Query Match   6.1%;   Score 73;   DB 5;   Length 526;
    Best Local Similarity   23.3%;   Pred. No. 41;
RESULT 925
ID   ADH42229 standard; protein; 526 AA
DE   Novel human protein NOV50d.
PN   WO2003102159-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
    Query Match   6.1%;   Score 73;   DB 8;   Length 526;
    Best Local Similarity   23.3%;   Pred. No. 41;
RESULT 926
ID   ABU31136 standard; protein; 553 AA.
DE   Protein encoded by Prokaryotic essential gene #16663.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
    Query Match   6.1%;   Score 73;   DB 6;   Length 553;
    Best Local Similarity   19.6%;   Pred. No. 44;
RESULT 927
ID   AAG24011 standard; protein; 556 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
PN   EP1033405-A2.
PD   06-SEP-2000.
    Query Match   6.1%;   Score 73;   DB 3;   Length 556;
    Best Local Similarity   22.0%;   Pred. No. 44;
RESULT 928
ID   ADQ96000 standard; protein; 608 AA.
DE   T cell activation associated protein #89.

PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
    Query Match   6.1%; Score 73; DB 8; Length 608;
    Best Local Similarity   19.5%; Pred. No. 50;
RESULT 929
ID ADR99134 standard; protein; 635 AA.
DE Human protein similar to yeast SSM4, TEB4, SEQ ID 140.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
    Query Match   6.1%; Score 73; DB 8; Length 635;
    Best Local Similarity   19.5%; Pred. No. 53;
RESULT 930
ID ABB71311 standard; protein; 717 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40725.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PBKE) PE CORP NY.
    Query Match   6.1%; Score 73; DB 4; Length 717;
    Best Local Similarity   21.3%; Pred. No. 62;
RESULT 931
ID AAW26673 standard; protein; 746 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIK) SMITHKLINE BEECHAM PLC.
    Query Match   6.1%; Score 73; DB 2; Length 746;
    Best Local Similarity   23.3%; Pred. No. 66;
RESULT 932
ID AAU37199 standard; protein; 748 AA.
DE Staphylococcus aureus cellular proliferation protein #1369.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   6.1%; Score 73; DB 4; Length 748;
    Best Local Similarity   23.3%; Pred. No. 66;
RESULT 933
ID AAW88407 standard; protein; 750 AA.
DE Human adult neural tissue secreted protein s195_10.
PN WO9857976-A1.
PD 23-DEC-1998.
PA (GMY) GENETICS INST INC.
    Query Match   6.1%; Score 73; DB 4; Length 750;
    Best Local Similarity   19.5%; Pred. No. 66;
RESULT 934
ID AAW26672 standard; protein; 788 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIK) SMITHKLINE BEECHAM PLC.
    Query Match   6.1%; Score 73; DB 2; Length 788;
    Best Local Similarity   23.3%; Pred. No. 71;
RESULT 935
ID ABU42392 standard; protein; 788 AA.
DE Protein encoded by Prokaryotic essential gene #27919.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   6.1%; Score 73; DB 6; Length 788;
    Best Local Similarity   23.3%; Pred. No. 71;
RESULT 936
ID AAU36734 standard; protein; 792 AA.
DE Staphylococcus aureus cellular proliferation protein #904.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   6.1%; Score 73; DB 4; Length 792;
    Best Local Similarity   23.3%; Pred. No. 72;
RESULT 937
ID ABJ19057 standard; protein; 792 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 334.
PN WO200259148-A2.

PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
    Query Match   6.1%; Score 73; DB 6; Length 792;
    Best Local Similarity   23.3%; Pred. No. 72;
RESULT 938
ID ABM73117 standard; protein; 792 AA.
DE Staphylococcus aureus protein #2357.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
    Query Match   6.1%; Score 73; DB 6; Length 792;
    Best Local Similarity   23.3%; Pred. No. 72;
RESULT 939
ID AAW68466 standard; protein; 845 AA.
DE Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
PN WO9825960-A1.
PD 18-JUN-1998.
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
    Query Match   6.1%; Score 73; DB 2; Length 845;
    Best Local Similarity   26.2%; Pred. No. 78;
RESULT 940
ID ADQ95946 standard; protein; 910 AA.
DE T cell activation associated protein #62.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
    Query Match   6.1%; Score 73; DB 8; Length 910;
    Best Local Similarity   19.5%; Pred. No. 87;
RESULT 941
ID ABG24246 standard; protein; 913 AA.
DE Novel human diagnostic protein #24237.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   6.1%; Score 73; DB 4; Length 913;
    Best Local Similarity   19.5%; Pred. No. 87;
RESULT 942
ID AAM51861 standard; protein; 966 AA.
DE Murine polycystic kidney disease protein 2.
PN WO200177331-A1.
PD 18-OCT-2001.
PA (MILL-) MILLENIUM PHARM INC.
    Query Match   6.1%; Score 73; DB 5; Length 966;
    Best Local Similarity   21.3%; Pred. No. 94;
RESULT 943
ID ABB07819 standard; protein; 966 AA.
DE Mouse polycystic kidney disease protein 2.
PN US2002035056-A1.
PD 21-MAR-2002.
PA (CURT/) CURTIS R A J.
    (SILO/) SILOS-SANTIAGO I.
    Query Match   6.1%; Score 73; DB 5; Length 966;
    Best Local Similarity   21.3%; Pred. No. 94;
RESULT 944
ID ADJ76159 standard; protein; 966 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1411.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
    Query Match   6.1%; Score 73; DB 8; Length 966;
    Best Local Similarity   21.3%; Pred. No. 94;
RESULT 945
ID ABG05866 standard; protein; 971 AA.
DE Novel human diagnostic protein #5857.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   6.1%; Score 73; DB 4; Length 971;
    Best Local Similarity   19.5%; Pred. No. 95;
RESULT 946
ID ADR99135 standard; protein; 971 AA.
DE Human protein similar to yeast SSM4, TEB4, SEQ ID 141.
PN WO2004078035-A2.

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PD   16-SEP-2004.
PA   (FARB ) BAYER PHARM CORP.
     Query Match             6.1%;  Score 73;  DB 8;  Length 971;
     Best Local Similarity   19.5%;            Pred. No. 95;
RESULT 947
ID   ABG07373 standard; protein; 976 AA.
DE   Novel human diagnostic protein #7364.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             6.1%;  Score 73;  DB 4;  Length 976;
     Best Local Similarity   19.5%;            Pred. No. 96;
RESULT 948
ID   ABU05456 standard; protein; 209 AA.
DE   M. tuberculosis and M. leprae marker protein #107.
PN   WO200274903-A2.
PD   26-SEP-2002.
PA   (INSP ) INST PASTEUR.
     Query Match             6.1%;  Score 72.5;  DB 5;  Length 209;
     Best Local Similarity   22.1%;              Pred. No. 13;
RESULT 949
ID   ABU15302 standard; protein; 222 AA.
DE   Protein encoded by Prokaryotic essential gene #829.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.1%;  Score 72.5;  DB 6;  Length 222;
     Best Local Similarity   20.5%;              Pred. No. 14;
RESULT 950
ID   ABB53879 standard; protein; 307 AA.
DE   Lactococcus lactis protein yfgG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
     Query Match             6.1%;  Score 72.5;  DB 5;  Length 307;
     Best Local Similarity   22.9%;              Pred. No. 22;
RESULT 951
ID   ABB53675 standard; protein; 325 AA.
DE   Lactococcus lactis protein ydhB.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
     Query Match             6.1%;  Score 72.5;  DB 5;  Length 325;
     Best Local Similarity   25.9%;              Pred. No. 24;
RESULT 952
ID   ADH87677 standard; protein; 353 AA.
DE   Enterococcus faecalis polypeptide #2157.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match             6.1%;  Score 72.5;  DB 7;  Length 353;
     Best Local Similarity   21.5%;              Pred. No. 27;
RESULT 953
ID   ADH87557 standard; protein; 359 AA.
DE   Enterococcus faecalis polypeptide #2037.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match             6.1%;  Score 72.5;  DB 7;  Length 359;
     Best Local Similarity   25.0%;              Pred. No. 27;
RESULT 954
ID   AAR37264 standard; protein; 389 AA.
DE   Oxytocin receptor.
PN   EP542424-A1.
PD   19-MAY-1993.
PA   (ROHT ) ROHTO PHARM CO LTD.
     Query Match             6.1%;  Score 72.5;  DB 2;  Length 389;
     Best Local Similarity   24.5%;              Pred. No. 31;
RESULT 955
ID   AAW23832 standard; protein; 389 AA.
DE   Human oxytocin receptor.

PN   EP811684-A2.
PD   10-DEC-1997.
PA   (ROHT.) ROHTO PHARM CO LTD.
     Query Match             6.1%;  Score 72.5;  DB 2;  Length 389;
     Best Local Similarity   24.5%;              Pred. No. 31;
RESULT 956
ID   AAM40217 standard; protein; 389 AA.
DE   Human polypeptide SEQ ID NO 3362.
PN   WO20153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             6.1%;  Score 72.5;  DB 4;  Length 389;
     Best Local Similarity   24.5%;              Pred. No. 31;
RESULT 957
ID   ABP81865 standard; protein; 389 AA.
DE   Human oxytocin receptor protein SEQ ID NO:215.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match             6.1%;  Score 72.5;  DB 6;  Length 389;
     Best Local Similarity   24.5%;              Pred. No. 31;
RESULT 958
ID   AAE38317 standard; protein; 389 AA.
DE   Human oxytocin receptor protein.
PN   WO200306402-A1.
PD   07-AUG-2003.
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
     Query Match             6.1%;  Score 72.5;  DB 6;  Length 389;
     Best Local Similarity   24.5%;              Pred. No. 31;
RESULT 959
ID   ADP12125 standard; protein; 389 AA.
DE   Human oxytocin receptor (OXTR) protein SEQ ID NO:2.
PN   WO200309816-A2.
PD   13-NOV-2003.
PA   (FARB ) BAYER AG.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 389;
     Best Local Similarity   24.5%;              Pred. No. 31;
RESULT 960
ID   ADI03915 standard; protein; 389 AA.
DE   Human oxytocin receptor polypeptide.
PN   WO2004000993-A2.
PD   31-DEC-2003.
PA   (UYQU-) UNIV QUEBEC A MONTREAL.
PA   (UYMO-) UNIV MONTREAL CENT HOSPITALIER.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 389;
     Best Local Similarity   24.5%;              Pred. No. 31;
RESULT 961
ID   ADO29590 standard; protein; 389 AA.
DE   Human GPCR OXTR, SEQ ID NO:692.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 389;
     Best Local Similarity   24.5%;              Pred. No. 31;
RESULT 962
ID   AAR58665 standard; protein; 448 AA.
DE   Bovine PACAP receptor type 1B mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             6.1%;  Score 72.5;  DB 2;  Length 448;
     Best Local Similarity   29.6%;              Pred. No. 37;
RESULT 963
ID   AAR58663 standard; protein; 476 AA.
DE   Bovine PACAP receptor type 1A mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             6.1%;  Score 72.5;  DB 2;  Length 476;
     Best Local Similarity   29.6%;              Pred. No. 40;
RESULT 964
ID   AARS8657 standard; protein; 485 AA.
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DE   Bovine PACAP receptor type 1B protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             6.1%;  Score 72.5;  DB 2;  Length 485;
     Best Local Similarity   29.6%;  Pred. No. 42;
RESULT 965
ID   AAR58655 standard; protein; 513 AA.
DE   Bovine PACAP receptor type 1A protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             6.1%;  Score 72.5;  DB 2;  Length 513;
     Best Local Similarity   29.6%;  Pred. No. 45;
RESULT 966
ID   ADN19765 standard; protein; 522 AA.
DE   Bacterial polypeptide #2418.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 522;
     Best Local Similarity   22.5%;  Pred. No. 46;
RESULT 967
ID   ADI81620 standard; protein; 769 AA.
DE   C. elegans protein similar to Pfam PF00023.
PN   US2004009537-A1.
PD   15-JAN-2004.
PA   (ROOS/) ROOS J.
PA   (STAU/) STAUDERMAN K.
PA   (VELI/) VELICELEBI G.
     Query Match             6.1%;  Score 72.5;  DB 8;  Length 769;
     Best Local Similarity   20.2%;  Pred. No. 79;
RESULT 968
ID   ABB05429 standard; protein; 848 AA.
DE   Arabidopsis thaliana ABH1 protein SEQ ID NO:2.
PN   WO200196585-A2.
PD   20-DEC-2001.
PA   (RBGC ) UNIV CALIFORNIA.
     Query Match             6.1%;  Score 72.5;  DB 5;  Length 848;
     Best Local Similarity   22.3%;  Pred. No. 90;
RESULT 969
ID   AAE31528 standard; protein; 848 AA.
DE   Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
PN   WO200281696-A2.
PD   17-OCT-2002.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
     Query Match             6.1%;  Score 72.5;  DB 6;  Length 848;
     Best Local Similarity   22.3%;  Pred. No. 90;
RESULT 970
ID   ABU25159 standard; protein; 851 AA.
DE   Protein encoded by Prokaryotic essential gene #10686.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.1%;  Score 72.5;  DB 6;  Length 851;
     Best Local Similarity   20.5%;  Pred. No. 91;
RESULT 971
ID   AAR34580 standard; protein; 3010 AA.
DE   Human hepatitis C virus gene encoded polypeptide.
PN   EP541089-A2.
PD   12-MAY-1993.
PA   (SANW ) SANWA KAGAKU KENKYUSHO CO.
     Query Match             6.1%;  Score 72.5;  DB 2;  Length 3010;
     Best Local Similarity   23.7%;  Pred. No. 5.2e+02;
RESULT 972
ID   ADQ96378 standard; protein; 208 AA.
DE   T cell activation associated protein #278.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match             6.0%;  Score 72;  DB 8;  Length 208;
     Best Local Similarity   20.8%;  Pred. No. 15;
RESULT 973
ID   ABB48543 standard; protein; 306 AA.
DE   Listeria monocytogenes protein #1247.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST PASTEUR.
     Query Match             6.0%;  Score 72;  DB 5;  Length 306;
     Best Local Similarity   21.0%;  Pred. No. 25;
RESULT 974
ID   ABU39432 standard; protein; 317 AA.
DE   Protein encoded by Prokaryotic essential gene #24959.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.0%;  Score 72;  DB 6;  Length 317;
     Best Local Similarity   23.5%;  Pred. No. 26;
RESULT 975
ID   AAB53392 standard; protein; 334 AA.
DE   Human colon cancer antigen protein sequence SEQ ID NO:932.
PN   WO200055351-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             6.0%;  Score 72;  DB 3;  Length 334;
     Best Local Similarity   28.8%;  Pred. No. 28;
RESULT 976
ID   AAY87505 standard; protein; 370 AA.
DE   Human G coupled-protein receptor, hGR3.
PN   WO200017641-A1.
PD   30-MAR-2000.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match             6.0%;  Score 72;  DB 3;  Length 370;
     Best Local Similarity   21.8%;  Pred. No. 33;
RESULT 977
ID   AAW20731 standard; protein; 375 AA.
DE   H. pylori inner membrane protein, 06cp1118orf6.
PN   WO960893-A1.
PD   19-DEC-1996.
PA   (ASTR ) ASTRA AB.
     Query Match             6.0%;  Score 72;  DB 2;  Length 375;
     Best Local Similarity   20.9%;  Pred. No. 33;
RESULT 978
ID   ABU19932 standard; protein; 396 AA.
DE   Protein encoded by Prokaryotic essential gene #5459.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             6.0%;  Score 72;  DB 6;  Length 396;
     Best Local Similarity   21.6%;  Pred. No. 36;
RESULT 979
ID   ABG25051 standard; protein; 414 AA.
DE   Novel human diagnostic protein #25042.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match             6.0%;  Score 72;  DB 4;  Length 414;
     Best Local Similarity   22.6%;  Pred. No. 38;
RESULT 980
ID   AAG50203 standard; protein; 427 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.0%;  Score 72;  DB 3;  Length 427;
     Best Local Similarity   22.0%;  Pred. No. 40;
RESULT 981
ID   AAG50202 standard; protein; 430 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match             6.0%;  Score 72;  DB 3;  Length 430;
     Best Local Similarity   22.0%;  Pred. No. 40;
```

RESULT 982
ID   ABM72825 standard; protein; 447 AA.
DE   Staphylococcus aureus protein #2065.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match   6.0%; Score 72; DB 6; Length 447;
     Best Local Similarity 23.9%; Pred. No. 42;

RESULT 983
ID   ABB62902 standard; protein; 448 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 15498.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.0%; Score 72; DB 4; Length 448;
     Best Local Similarity 25.1%; Pred. No. 43;

RESULT 984
ID   ABJ18913 standard; protein; 453 AA.
DE   Pathogen specific antigen related staphylococcal protein SEQ ID No 59.
PN   WO200259148-A2.
PD   01-AUG-2002.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
     Query Match   6.0%; Score 72; DB 6; Length 453;
     Best Local Similarity 23.9%; Pred. No. 43;

RESULT 985
ID   ABU16441 standard; protein; 453 AA.
DE   Protein encoded by Prokaryotic essential gene #1968.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.0%; Score 72; DB 6; Length 453;
     Best Local Similarity 23.9%; Pred. No. 43;

RESULT 986
ID   ADN73057 standard; protein; 468 AA.
DE   Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
PN   WO2004035798-A2.
PD   29-APR-2004.
PA   (CROP-) CROPDESIGN NV.
     Query Match   6.0%; Score 72; DB 8; Length 468;
     Best Local Similarity 21.8%; Pred. No. 45;

RESULT 987
ID   AAG16338 standard; protein; 495 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 72; DB 3; Length 495;
     Best Local Similarity 21.3%; Pred. No. 49;

RESULT 988
ID   AAG16337 standard; protein; 497 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 72; DB 3; Length 497;
     Best Local Similarity 21.3%; Pred. No. 49;

RESULT 989
ID   AAG16336 standard; protein; 507 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 72; DB 3; Length 507;
     Best Local Similarity 21.3%; Pred. No. 51;

RESULT 990
ID   ADS23568 standard; protein; 543 AA.
DE   Bacterial polypeptide #12601.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.0%; Score 72; DB 8; Length 543;
     Best Local Similarity 18.6%; Pred. No. 56;

RESULT 991
ID   ABU25738 standard; protein; 552 AA.
DE   Protein encoded by Prokaryotic essential gene #11265.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.0%; Score 72; DB 6; Length 552;
     Best Local Similarity 19.5%; Pred. No. 57;

RESULT 992
ID   AAG50201 standard; protein; 556 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 72; DB 3; Length 556;
     Best Local Similarity 22.0%; Pred. No. 58;

RESULT 993
ID   ADJ69383 standard; protein; 594 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1189.
PN   WO200308768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match   6.0%; Score 72; DB 7; Length 594;
     Best Local Similarity 20.8%; Pred. No. 63;

RESULT 994
ID   ABP97202 standard; protein; 696 AA.
DE   Tumour-associated antigenic target protein TAT247 SEQ ID NO:84.
PN   WO2003024392-A2.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.0%; Score 72; DB 6; Length 696;
     Best Local Similarity 20.8%; Pred. No. 79;

RESULT 995
ID   ABP97201 standard; protein; 696 AA.
DE   Tumour-associated antigenic target protein TAT225 SEQ ID NO:83.
PN   WO2003024392-A2.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.0%; Score 72; DB 6; Length 696;
     Best Local Similarity 20.8%; Pred. No. 79;

RESULT 996
ID   ABP81969 standard; protein; 696 AA.
DE   Human GPCR XPR1 protein SEQ ID NO:424.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   6.0%; Score 72; DB 6; Length 696;
     Best Local Similarity 20.8%; Pred. No. 79;

RESULT 997
ID   ADB67652 standard; protein; 696 AA.
DE   Human xenotropic& polytropic retrovirus receptor, SEQ ID 21.
PN   WO2003072824-A1.
PD   04-SEP-2003.
PA   (SANY) SANKYO CO LTD.
     Query Match   6.0%; Score 72; DB 7; Length 696;
     Best Local Similarity 20.8%; Pred. No. 79;

RESULT 998
ID   ADQ96380 standard; protein; 696 AA.
DE   T cell activation associated protein #279.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match   6.0%; Score 72; DB 8; Length 696;
     Best Local Similarity 20.8%; Pred. No. 79;

RESULT 999
ID   ABM69179 standard; protein; 724 AA.
DE   Photorhabdus luminescens protein sequence #2276.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   6.0%; Score 72; DB 6; Length 724;
     Best Local Similarity 21.3%; Pred. No. 83;

RESULT 1000
ID   AAB46702 standard; protein; 741 AA.
DB   P. falciparum DNA polymerase protein fragment SEQ ID NO 11.
PN   WO20007535-A2.
PD   14-DEC-2000.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   6.0%; Score 72; DB 4; Length 741;
     Best Local Similarity 30.4%; Pred. No. 86;

RESULT 1001
ID   AAM47977 standard; protein; 788 AA.
DB   Human hARRG.
PN   CN1315342-A.
PD   03-OCT-2001.
PA   (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
     Query Match   6.0%; Score 72; DB 5; Length 788;
     Best Local Similarity 26.3%; Pred. No. 93;

RESULT 1002
ID   ABB58917 standard; protein; 1275 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 3543.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.0%; Score 72; DB 4; Length 1275;
     Best Local Similarity 19.0%; Pred. No. 1.8e+02;

RESULT 1003
ID   AAY70064 standard; protein; 2307 AA.
DB   Recombinant fusion pHCAP-1 polyprotein.
PN   WO20008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match   6.0%; Score 72; DB 3; Length 2307;
     Best Local Similarity 23.6%; Pred. No. 4.1e+02;

RESULT 1004
ID   AAY70065 standard; protein; 2307 AA.
DB   Recombinant fusion pHCAP-3 polyprotein.
PN   WO20008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match   6.0%; Score 72; DB 3; Length 2307;
     Best Local Similarity 23.6%; Pred. No. 4.1e+02;

RESULT 1005
ID   AAY70066 standard; protein; 2307 AA.
DB   Recombinant fusion pHCAP-4 polyprotein.
PN   WO20008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match   6.0%; Score 72; DB 3; Length 2307;
     Best Local Similarity 23.6%; Pred. No. 4.1e+02;

RESULT 1006
ID   AAM93791 standard; protein; 208 AA.
DB   Human polypeptide, SEQ ID NO: 3817.
PN   EP1396543-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
     Query Match   6.0%; Score 71.5; DB 4; Length 208;
     Best Local Similarity 25.2%; Pred. No. 17;

RESULT 1007
ID   ADL31784 standard; protein; 208 AA.
DB   Human protein encoded by a full length cDNA clone SeqID 3817.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match   6.0%; Score 71.5; DB 8; Length 208;
     Best Local Similarity 25.2%; Pred. No. 17;

RESULT 1008
ID   AAG56417 standard; protein; 209 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 71.5; DB 3; Length 209;
     Best Local Similarity 25.6%; Pred. No. 17;

RESULT 1009
ID   AAG56416 standard; protein; 216 AA.

DE   Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 71.5; DB 3; Length 216;
     Best Local Similarity 25.6%; Pred. No. 18;

RESULT 1010
ID   AAG16922 standard; protein; 218 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 71.5; DB 3; Length 218;
     Best Local Similarity 42.4%; Pred. No. 18;

RESULT 1011
ID   ABB53486 standard; protein; 301 AA.
DE   Lactococcus lactis protein ybiG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
     Query Match   6.0%; Score 71.5; DB 5; Length 301;
     Best Local Similarity 26.5%; Pred. No. 28;

RESULT 1012
ID   AAW37976 standard; protein; 342 AA.
DE   Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
PN   WO9815289-A1.
PD   16-APR-1998.
PA   (CORR) CORNELL RES FOUND INC.
     Query Match   6.0%; Score 71.5; DB 2; Length 342;
     Best Local Similarity 22.2%; Pred. No. 34;

RESULT 1013
ID   ADG87423 standard; protein; 348 AA.
DE   Meloidogyne incognita plk1 protein.
PN   US200315 0017-A1.
PD   07-AUG-2003.
PA   (MESA/) MESA J R B.
PA   (GRAH/) GRAHAM M W.
PA   (FAIR/) FAIRBAIRN D J.
     Query Match   6.0%; Score 71.5; DB 7; Length 348;
     Best Local Similarity 21.0%; Pred. No. 34;

RESULT 1014
ID   ADR40542 standard; protein; 363 AA.
DE   Ovine ML1A protein.
PN   US200416 1823-A1.
PD   19-AUG-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
     Query Match   6.0%; Score 71.5; DB 8; Length 363;
     Best Local Similarity 23.1%; Pred. No. 36;

RESULT 1015
ID   AAR88410 standard; protein; 366 AA.
DE   High-affinity melatonin-1a receptor.
PN   WO9535320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
     Query Match   6.0%; Score 71.5; DB 2; Length 366;
     Best Local Similarity 23.1%; Pred. No. 37;

RESULT 1016
ID   ABU03456 standard; protein; 382 AA.
DE   Angiogenesis-associated human protein sequence #1.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match   6.0%; Score 71.5; DB 6; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;

RESULT 1017
ID   ABP58069 standard; protein; 382 AA.
DE   Human G-protein coupled receptor GAVE1.
PN   WO200295056-A2.
PD   28-NOV-2002.
PA   (AVET) AVENTIS PHARM INC.
     Query Match   6.0%; Score 71.5; DB 6; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;

RESULT 1018
ID   ABP59277 standard; protein; 382 AA.
DE   Human Edg1 receptor.
PN   WO2003006503-A1.
PD   23-JAN-2003.
PA   (CERE-) CERETEK.
     Query Match   6.0%; Score 71.5; DB 6; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1019
ID   ABU08809 standard; protein; 382 AA.
DE   Human EDG-1 protein.
PN   US2002155512-A1.
PD   24-OCT-2002.
PA   (RIGE-) RIGEL PHARM INC.
     Query Match   6.0%; Score 71.5; DB 6; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1020
ID   ABR59701 standard; protein; 382 AA.
DE   Human endothelial differentiation sphingolipid GPCR 1.
PN   WO2003029277-A2.
PD   10-APR-2003.
PA   (RIGE-) RIGEL PHARM INC.
     Query Match   6.0%; Score 71.5; DB 6; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1021
ID   ABP81876 standard; protein; 382 AA.
DE   Human sphingolipid receptor Edg1 protein SEQ ID NO:237.
PN   WO2002061087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   6.0%; Score 71.5; DB 6; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1022
ID   ADB67662 standard; protein; 382 AA.
DE   Human EDG1, SEQ ID 31.
PN   WO2003072824-A1.
PD   04-SEP-2003.
PA   (SANY) SANKYO CO LTD.
     Query Match   6.0%; Score 71.5; DB 7; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1023
ID   ADC40477 standard; protein; 382 AA.
DE   Protein of human EDG-1.
PN   WO2003052096-A1.
PD   26-JUN-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   6.0%; Score 71.5; DB 7; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1024
ID   ADN38684 standard; protein; 382 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:2.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match   6.0%; Score 71.5; DB 7; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1025
ID   ABM85457 standard; protein; 382 AA.
DE   Human protein sequence hCP1630135.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
     Query Match   6.0%; Score 71.5; DB 7; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1026
ID   ADJ45541 standard; protein; 382 AA.
DE   LXR-ligand induced transcript seq id 72.
PN   US2004022276-A1.
PD   05-FEB-2004.
PA   (WARD/) WARD T R.
PA   (MAOM/) MAO M.
PA   (LINS/) LINSLEY P S.
PA   (LUND/) LUND E.
     Query Match   6.0%; Score 71.5; DB 8; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1027
ID   ADR67022 standard; protein; 382 AA.
DE   Human cancer associated protein sequence SEQ ID NO:68.
PN   WO2004074321-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match   6.0%; Score 71.5; DB 8; Length 382;
     Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1028
ID   ADN19614 standard; protein; 383 AA.
DE   Bacterial polypeptide #2267.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   6.0%; Score 71.5; DB 8; Length 383;
     Best Local Similarity 22.0%; Pred. No. 39;
RESULT 1029
ID   ABB05226 standard; protein; 390 AA.
DE   Catostomus commersoni isotocin receptor protein SEQ ID NO:3.
PN   WO2001092296-A2.
PD   06-DEC-2001.
PA   (FARB) BAYER AG.
     Query Match   6.0%; Score 71.5; DB 5; Length 390;
     Best Local Similarity 22.2%; Pred. No. 40;
RESULT 1030
ID   ADM83141 standard; protein; 394 AA.
DE   Rat vesicle membrane protein (VMP)2.
PN   US2003175787-A1.
PD   18-SEP-2003.
PA   (INCY-) INCYTE CORP.
     Query Match   6.0%; Score 71.5; DB 7; Length 394;
     Best Local Similarity 22.7%; Pred. No. 41;
RESULT 1031
ID   ABB48023 standard; protein; 435 AA.
DE   Listeria monocytogenes protein #727.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
     Query Match   6.0%; Score 71.5; DB 5; Length 435;
     Best Local Similarity 21.4%; Pred. No. 47;
RESULT 1032
ID   AAR22000 standard; protein; 441 AA.
DE   Partial M17 antigen from Region II, encoded by PCR prod.
PN   WO9203457-A.
PD   05-MAR-1992.
PA   (REGC) UNIV CALIFORNIA.
     Query Match   6.0%; Score 71.5; DB 2; Length 441;
     Best Local Similarity 22.6%; Pred. No. 48;
RESULT 1033
ID   ABP75877 standard; protein; 470 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 1061.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   6.0%; Score 71.5; DB 6; Length 470;
     Best Local Similarity 22.4%; Pred. No. 52;
RESULT 1034
ID   ABU26033 standard; protein; 524 AA.
DE   Protein encoded by Prokaryotic essential gene #11560.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.0%; Score 71.5; DB 6; Length 524;
     Best Local Similarity 26.6%; Pred. No. 61;
RESULT 1035
ID   ABJ37074 standard; protein; 565 AA.
DE   Human breast cancer / ovarian cancer related protein #50.

PN   WO2003000012-A2.
PD   03-JAN-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   6.0%; DB 6;   Length 565;
     Best Local Similarity 22.4%; Pred. No. 67;
RESULT 1036
ID   AAW51244 standard; protein; 568 AA.
DE   Human calcitonin receptor.
PN   WO982124-A1.
PD   22-MAY-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   6.0%; DB 2;   Length 568;
     Best Local Similarity 22.4%; Pred. No. 68;
RESULT 1037
ID   ABU16392 standard; protein; 603 AA.
DE   Protein encoded by Prokaryotic essential gene #1919.
PN   WO20027183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.0%; DB 6;   Length 603;
     Best Local Similarity 21.3%; Pred. No. 74;
RESULT 1038
ID   ABM72619 standard; protein; 603 AA.
DE   Staphylococcus aureus protein #1859.
PN   WO20294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match   6.0%; DB 6;   Length 603;
     Best Local Similarity 21.3%; Pred. No. 74;
RESULT 1039
ID   ADM43215 standard; protein; 697 AA.
DE   Human methionine synthase reductase del Arg 559 variant.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; DB 7;   Length 697;
     Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1040
ID   ADM43217 standard; protein; 697 AA.
DE   Human methionine synthase reductase del Leu 576 variant.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; DB 7;   Length 697;
     Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1041
ID   AAB07591 standard; protein; 698 AA.
DE   A human methionine synthase reductase polypeptide.
PN   WO20004196-A2.
PD   20-JUL-2000.
PA   (UYMC-) UNIV MCGILL.
     Query Match   6.0%; DB 3;   Length 698;
     Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1042
ID   ABG00883 standard; protein; 698 AA.
DE   Novel human diagnostic protein #874.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   6.0%; DB 4;   Length 698;
     Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1043
ID   ADM43211 standard; protein; 698 AA.
DE   Human methionine synthase reductase Met22Ile variant.
PN   US2003082676-A1.

PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; DB 7;   Length 698;
     Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1044
ID   ADM43213 standard; protein; 698 AA.
DE   Human methionine synthase reductase Cys37Tyr variant.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; DB 7;   Length 698;
     Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1045
ID   ADM43207 standard; protein; 698 AA.
DE   Human wild-type methionine synthase reductase.
PN   US2003082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%; DB 7;   Length 698;
     Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1046
ID   ADQ39857 standard; protein; 698 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   6.0%; DB 8;   Length 698;
     Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1047
ID   ADQ39858 standard; protein; 725 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1521.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   6.0%; DB 8;   Length 725;
     Best Local Similarity 22.8%; Pred. No. 95;
RESULT 1048
ID   AAY51606 standard; protein; 890 AA.
DE   Human wml protein.
PN   DE1945277-C1.
PD   09-MAR-2000.
PA   (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
     Query Match   6.0%; DB 3;   Length 890;
     Best Local Similarity 23.8%; Pred. No. 1.3e+02;
RESULT 1049
ID   ABB78282 standard; protein; 890 AA.
DE   Amino acid sequence of human wolframin polypeptide.
PN   WO20026307-A2.
PD   15-AUG-2002.
PA   (PHAA-) PHARMACIA & UPJOHN CO.
     Query Match   6.0%; DB 5;   Length 890;
     Best Local Similarity 23.8%; Pred. No. 1.3e+02;
RESULT 1050
ID   ADD46013 standard; protein; 890 AA.
DE   Human Protein 076024, SEQ ID NO 11685.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   6.0%; DB 7;   Length 890;
     Best Local Similarity 23.8%; Pred. No. 1.3e+02;

RESULT 1051
ID ADF69127 standard; protein; 890 AA.
DE Human MP53 protein sequence SEQ ID NO:97.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
  Query Match   6.0%; Score 71.5; DB 7; Length 890;
  Best Local Similarity 23.8%; Pred. No. 1.3e+02;

RESULT 1052
ID ADL22689 standard; protein; 2245 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 138.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match   6.0%; Score 71.5; DB 7; Length 2245;
  Best Local Similarity 22.4%; Pred. No. 4.6e+02;

RESULT 1053
ID AAB42192 standard; protein; 2405 AA.
DE Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
  Query Match   6.0%; Score 71.5; DB 3; Length 2405;
  Best Local Similarity 22.4%; Pred. No. 5e+02;

RESULT 1054
ID ABB11404 standard; peptide; 2560 AA.
DE Human FLAMINGO 1 homologue, SEQ ID NO:1774.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSB-) HYSEQ INC.
  Query Match   6.0%; Score 71.5; DB 4; Length 2560;
  Best Local Similarity 22.4%; Pred. No. 5.5e+02;

RESULT 1055
ID ABU11556 standard; protein; 2894 AA.
DE Human MDDT polypeptide SEQ ID 503.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match   6.0%; Score 71.5; DB 6; Length 2894;
  Best Local Similarity 22.4%; Pred. No. 6.5e+02;

RESULT 1056
ID AAU07054 standard; protein; 2923 AA.
DE Human Flamingo protein encoded by cDNA splice variant.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
  Query Match   6.0%; Score 71.5; DB 4; Length 2923;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1057
ID AAM50866 standard; protein; 2923 AA.
DE Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
PN WO200208765-A2.
PD 31-JAN-2002.
PA (GENO-) APPLIED GENOMICS INC.
  Query Match   6.0%; Score 71.5; DB 5; Length 2923;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1058
ID ABP82018 standard; protein; 2923 AA.
DE Human GPCR CELSR2 protein SEQ ID NO:524.
PN US2003086934-A1.
PD 08-MAY-2003.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
  Query Match   6.0%; Score 71.5; DB 6; Length 2923;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1059
ID ADC15499 standard; protein; 2923 AA.
DE Human cadherin EGF LAG seven-pass G-type receptor 2.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (STRD) UNIV STANFORD.
PA (BOTS/) BOTSTEIN D.
PA (BROW/) BROWN P O.
PA (PERO/) PEROU C M.
PA (RING/) RING B.
PA (ROSS/) ROSS D.
PA (SBIT/) SEITZ R.
PA (VRIJ/) VAN DE RIJN J M.
  Query Match   6.0%; Score 71.5; DB 7; Length 2923;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1060
ID ADC86479 standard; protein; 2923 AA.
DE Human GPCR protein SEQ ID NO:932.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
  Query Match   6.0%; Score 71.5; DB 7; Length 2923;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1061
ID ADE54407 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 210.
PN WO200316475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
  Query Match   6.0%; Score 71.5; DB 7; Length 2923;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1062
ID ADE54411 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 214.
PN WO200316475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
  Query Match   6.0%; Score 71.5; DB 7; Length 2923;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1063
ID AD029245 standard; protein; 2923 AA.
DE Human GPCR CELSR2, SEQ ID NO:346.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
  Query Match   6.0%; Score 71.5; DB 8; Length 2923;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1064
ID AAU74826 standard; protein; 2936 AA.
DE Human REPTR 9 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match   6.0%; Score 71.5; DB 5; Length 2936;
  Best Local Similarity 22.4%; Pred. No. 6.6e+02;

RESULT 1065
ID AAU07053 standard; protein; 2956 AA.
DE Human Flamingo polypeptide.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
  Query Match   6.0%; Score 71.5; DB 4; Length 2956;
  Best Local Similarity 22.4%; Pred. No. 6.7e+02;

RESULT 1066
ID AAR34468 standard; protein; 3011 AA.
DE Encoded by full-length Hepatitis C virus clone JK1-B.
PN JP05068562-A.
PD 23-MAR-1993.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
  Query Match   6.0%; Score 71.5; DB 2; Length 3011;
  Best Local Similarity 23.7%; Pred. No. 6.9e+02;

RESULT 1067
ID AAR31621 standard; protein; 3011 AA.
DE Hepatitis C virus (HCV) polyprotein.
PN WO930365-A2.
PD 07-JAN-1993.
PA (CHIR) CHIRON CORP.
  Query Match   6.0%; Score 71.5; DB 2; Length 3011;
  Best Local Similarity 22.8%; Pred. No. 6.9e+02;

RESULT 1068
ID   ABB67866 standard; protein; 5303 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 30390.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.0%; Score 71.5; DB 4; Length 5303;
     Best Local Similarity 29.5%; Pred. No. 1.5e+03;
RESULT 1069
ID   ABB06793 standard; protein; 198 AA.
DE   Human transmembrane 4 protein 22 SEQ ID NO:2.
PN   CN1327990-A.
PD   26-DEC-2001.
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
     Query Match   5.9%; Score 71; DB 5; Length 198;
     Best Local Similarity 24.5%; Pred. No. 18;
RESULT 1070
ID   ABR58398 standard; protein; 240 AA.
DE   Human NOV17a.
PN   WO2003029423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.9%; Score 71; DB 6; Length 240;
     Best Local Similarity 18.6%; Pred. No. 24;
RESULT 1071
ID   ABP26255 standard; protein; 295 AA.
DE   Streptococcus polypeptide SEQ ID NO 1686.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match   5.9%; Score 71; DB 5; Length 295;
     Best Local Similarity 24.9%; Pred. No. 31;
RESULT 1072
ID   AAG72952 standard; protein; 310 AA.
DE   Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
     Query Match   5.9%; Score 71; DB 4; Length 310;
     Best Local Similarity 22.9%; Pred. No. 34;
RESULT 1073
ID   AAR48717 standard; protein; 312 AA.
DE   G-protein coupled human interleukin-8 receptor protein.
PN   WO9405695-A1.
PD   17-MAR-1994.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   5.9%; Score 71; DB 2; Length 312;
     Best Local Similarity 22.9%; Pred. No. 34;
RESULT 1074
ID   AAW02689 standard; peptide; 312 AA.
DE   G-protein coupled human interleukin-8 receptor.
PN   US5508384-A.
PD   16-APR-1996.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   5.9%; Score 71; DB 2; Length 312;
     Best Local Similarity 19.7%; Pred. No. 34;
RESULT 1075
ID   AAG72169 standard; protein; 312 AA.
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1850.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
     Query Match   5.9%; Score 71; DB 4; Length 312;
     Best Local Similarity 19.7%; Pred. No. 34;
RESULT 1076
ID   AAG72377 standard; protein; 312 AA.
DE   Human OR-like polypeptide query sequence, SEQ ID NO: 2058.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.

PA   (YEDA) YEDA RES & DEV CO LTD.
     Query Match   5.9%; Score 71; DB 4; Length 312;
     Best Local Similarity 22.9%; Pred. No. 34;
RESULT 1077
ID   ABB54394 standard; protein; 391 AA.
DE   Lactococcus lactis protein yкII.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
     Query Match   5.9%; Score 71; DB 5; Length 391;
     Best Local Similarity 20.3%; Pred. No. 46;
RESULT 1078
ID   ABB48413 standard; protein; 423 AA.
DE   Listeria monocytogenes protein #1117.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
     Query Match   5.9%; Score 71; DB 5; Length 423;
     Best Local Similarity 28.4%; Pred. No. 52;
RESULT 1079
ID   ADL05302 standard; protein; 423 AA.
DE   M. catarrhalis protein #1068.
PN   US6673910-B1.
PD   06-JAN-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.9%; Score 71; DB 8; Length 423;
     Best Local Similarity 38.0%; Pred. No. 52;
RESULT 1080
ID   ADJ95142 standard; protein; 444 AA.
DE   Novel NOVX protein sequence #185.
PN   WO200304025-A2.
PD   15-MAY-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.9%; Score 71; DB 7; Length 444;
     Best Local Similarity 21.0%; Pred. No. 55;
RESULT 1081
ID   ADJ95144 standard; protein; 444 AA.
DE   Novel NOVX protein sequence #186.
PN   WO200304025-A2.
PD   15-MAY-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.9%; Score 71; DB 7; Length 444;
     Best Local Similarity 21.0%; Pred. No. 55;
RESULT 1082
ID   ADP29417 standard; protein; 455 AA.
DE   Human secreted protein SEQ ID #184.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
     Query Match   5.9%; Score 71; DB 8; Length 455;
     Best Local Similarity 24.3%; Pred. No. 57;
RESULT 1083
ID   ABU19912 standard; protein; 457 AA.
DE   Protein encoded by Prokaryotic essential gene #5439.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.9%; Score 71; DB 6; Length 457;
     Best Local Similarity 22.0%; Pred. No. 57;
RESULT 1084
ID   ADI24575 standard; protein; 470 AA.
DE   Human endogenous 5HT2A serotonin receptor.
PN   US200322442-A1.
PD   04-DEC-2003.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
PA   (LIAW/) LIAW C W.
PA   (RUSS/) RUSSO J F.
PA   (THOM/) THOMSEN W J.
     Query Match   5.9%; Score 71; DB 8; Length 470;
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1085
ID   AAR37659 standard; protein; 471 AA.

DE   Sequence encoded by cDNA.
PN   WO9311257-A2.
PD   10-JUN-1993.
PA   (BOEH) BOEHRINGER INGELHEIM INT GMBH.
     Query Match   5.9%; Score 71; DB 2; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1086
ID   AAW23781 standard; protein; 471 AA.
DE   Human serotonin 5-HT2 receptor protein.
PN   US5561024-A.
PD   26-AUG-1997.
PA   (SYNA-) SYNAPTIC PHARM CORP.
     Query Match   5.9%; Score 71; DB 2; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1087
ID   AAW77107 standard; protein; 471 AA.
DE   Human 5-HT2A serotonin receptor.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.
     Query Match   5.9%; Score 71; DB 2; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1088
ID   AAY90640 standard; protein; 471 AA.
DE   Human G protein-coupled receptor 5HT-2A (serotonin receptor).
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%; Score 71; DB 3; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1089
ID   AAY90675 standard; protein; 471 AA.
DE   Human mutant G protein-coupled receptor 5HT-2A.
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%; Score 71; DB 3; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1090
ID   ABB07978 standard; protein; 471 AA.
DE   Human 5-HT2 receptor sequence.
PN   US6383762-B1.
PD   07-MAY-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.
     Query Match   5.9%; Score 71; DB 5; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1091
ID   ABP81765 standard; protein; 471 AA.
DE   Human 5-HT2A receptor protein SEQ ID NO:12.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   5.9%; Score 71; DB 6; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1092
ID   ADC22641 standard; protein; 471 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #32.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%; Score 71; DB 7; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1093
ID   ADC22747 standard; protein; 471 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #72.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%; Score 71; DB 7; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1094

ID   ADE65844 standard; protein; 471 AA.
DE   Human serotonin 2A receptor.
PN   US2003170723-A1.
PD   11-SEP-2003.
PA   (SATO/) SATO T.
     Query Match   5.9%; Score 71; DB 7; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1095
ID   ADH14220 standard; protein; 471 AA.
DE   Mutated human serotonin 5HT_2A.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match   5.9%; Score 71; DB 7; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1096
ID   ADH14114 standard; protein; 471 AA.
DE   Human serotonin 5HT_2A.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match   5.9%; Score 71; DB 7; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1097
ID   ADL90125 standard; protein; 471 AA.
DE   Human serotonin receptor 5HT2a.
PN   US2003167476-A1.
PD   04-SEP-2003.
PA   (CONK/) CONKLIN B R.
     Query Match   5.9%; Score 71; DB 7; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1098
ID   ADQ29506 standard; protein; 471 AA.
DE   Human GPCR HTR2A, SEQ ID NO:608.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match   5.9%; Score 71; DB 8; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1099
ID   ADQ39800 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1463.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   5.9%; Score 71; DB 8; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1100
ID   ADQ39799 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1462.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   5.9%; Score 71; DB 8; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1101
ID   ADQ39798 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1461.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   5.9%; Score 71; DB 8; Length 471
     Best Local Similarity 23.7%; Pred. No. 60;
RESULT 1102
ID   AAY01626 standard; protein; 478 AA.
DE   Amino acid sequence of the human 5-HT2 receptor.
PN   US5585785-A.
PD   23-MAR-1999.
PA   (SYNA-) SYNAPTIC PHARM CORP.

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Query Match            5.9%;   Score 71;   DB 2;   Length 478;
Best Local Similarity  23.7%;  Pred. No. 61;
RESULT 1103
ID  ABG70577 standard; protein; 480 AA.
DE  Human serotonin (5-HT2) receptor.
PN  US2002098548-A1.
PD  25-JUL-2002.
PA  (SYNA-) SYNAPTIC PHARM CORP.
Query Match            5.9%;   Score 71;   DB 5;   Length 480;
Best Local Similarity  23.7%;  Pred. No. 62;
RESULT 1104
ID  ABM70440 standard; protein; 493 AA.
DE  Photorhabdus luminescens protein sequence #3537.
PN  WO200294867-A2.
PD  28-NOV-2002.
PA  (INSP ) INST PASTEUR.
PA  (CNRS ) CNRS CENT NAT RECH SCI.
Query Match            5.9%;   Score 71;   DB 6;   Length 493;
Best Local Similarity  23.5%;  Pred. No. 64;
RESULT 1105
ID  ADB56383 standard; protein; 545 AA.
DE  Rat Protein 070536, SEQ ID NO 2235.
PN  WO2003016475-A2.
PD  27-FEB-2003.
PA  (GEHO ) GEN HOSPITAL CORP.
PA  (FARB ) BAYER AG.
Query Match            5.9%;   Score 71;   DB 7;   Length 545;
Best Local Similarity  22.0%;  Pred. No. 73;
RESULT 1106
ID  ADD48660 standard; protein; 545 AA.
DE  Rat Protein BAA25372, SEQ ID NO 14366.
PN  WO2003016475-A2.
PD  27-FEB-2003.
PA  (GEHO ) GEN HOSPITAL CORP.
PA  (FARB ) BAYER AG.
Query Match            5.9%;   Score 71;   DB 7;   Length 545;
Best Local Similarity  22.0%;  Pred. No. 73;
RESULT 1107
ID  ADS43584 standard; protein; 546 AA.
DE  Bacterial polypeptide #22014.
PN  US2003223675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.
Query Match            5.9%;   Score 71;   DB 8;   Length 546;
Best Local Similarity  26.2%;  Pred. No. 74;
RESULT 1108
ID  ABU26399 standard; protein; 559 AA.
DE  Aspergillus fumigatus essential gene protein #1057.
PN  WO200286090-A2.
PD  31-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
Query Match            5.9%;   Score 71;   DB 5;   Length 559;
Best Local Similarity  23.1%;  Pred. No. 76;
RESULT 1109
ID  ABP35686 standard; protein; 563 AA.
DE  Fungal ZBC protein sequence #112.
PN  WO200224865-A2.
PD  28-MAR-2002.
PA  (MICR-) MICROBIA INC.
Query Match            5.9%;   Score 71;   DB 6;   Length 563;
Best Local Similarity  19.1%;  Pred. No. 77;
RESULT 1110
ID  AAB20578 standard; protein; 564 AA.
DE  Mouse OCTN3 protein SEQ ID NO:1.
PN  WO200046368-A1.
PD  10-AUG-2000.
PA  (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match            5.9%;   Score 71;   DB 3;   Length 564;
Best Local Similarity  21.4%;  Pred. No. 77;

RESULT 1111
ID  ADQ96374 standard; protein; 631 AA.
DE  T cell activation associated protein #276.
PN  WO2004058805-A2.
PD  15-JUL-2004.
PA  (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match            5.9%;   Score 71;   DB 8;   Length 631;
Best Local Similarity  21.3%;  Pred. No. 90;
RESULT 1112
ID  ADQ96376 standard; protein; 631 AA.
DE  T cell activation associated protein #277.
PN  WO2004058805-A2.
PD  15-JUL-2004.
PA  (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match            5.9%;   Score 71;   DB 8;   Length 631;
Best Local Similarity  21.3%;  Pred. No. 90;
RESULT 1113
ID  ABB91532 standard; protein; 676 AA.
DE  Herbicidally active polypeptide SEQ ID NO 743.
PN  WO200210210-A2.
PD  07-FEB-2002.
PA  (FARB ) BAYER AG.
Query Match            5.9%;   Score 71;   DB 5;   Length 676;
Best Local Similarity  22.3%;  Pred. No. 99;
RESULT 1114
ID  AAE21800 standard; protein; 727 AA.
DE  Human HIPHUM 0000029 protein.
PN  GB2365432-A.
PD  20-FEB-2002.
PA  (GLAX ) GLAXO GROUP LTD.
Query Match            5.9%;   Score 71;   DB 5;   Length 727;
Best Local Similarity  24.3%;  Pred. No. 1.1e+02;
RESULT 1115
ID  ABU54636 standard; protein; 727 AA.
DE  Human NOVX polypeptide #95.
PN  WO200281498-A2.
PD  17-OCT-2002.
PA  (CURA-) CURAGEN CORP.
Query Match            5.9%;   Score 71;   DB 6;   Length 727;
Best Local Similarity  24.3%;  Pred. No. 1.1e+02;
RESULT 1116
ID  ADH76500 standard; protein; 727 AA.
DE  727 amino acid human neurotransmitter transporter protein.
PN  US2003219774-A1.
PD  27-NOV-2003.
PA  (SHAR/) SHARMA R.
PA  (RAMA/) RAMANATHAN C S.
PA  (WEST/) WESTPHAL R.
PA  (FEDE/) FEDER J N.
PA  (LEEL/) LEE L M.
Query Match            5.9%;   Score 71;   DB 8;   Length 727;
Best Local Similarity  24.3%;  Pred. No. 1.1e+02;
RESULT 1117
ID  ABR62929 standard; protein; 744 AA.
DE  Human neurotransmitter transporter.
PN  WO2003059947-A1.
PD  24-JUL-2003.
PA  (FARB ) BAYER AG.
Query Match            5.9%;   Score 71;   DB 7;   Length 744;
Best Local Similarity  24.3%;  Pred. No. 1.1e+02;
RESULT 1118
ID  ABB60052 standard; protein; 792 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 6948.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE ) PE CORP NY.
Query Match            5.9%;   Score 71;   DB 4;   Length 792;
Best Local Similarity  17.7%;  Pred. No. 1.2e+02;
RESULT 1119
ID  AAR30616 standard; protein; 3010 AA.
DE  Polypeptide coded by Korean HCV full cDNA sequence LBC1.
PN  EP523318-A2.
PD  07-JAN-1993.
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PA   (LUCK-) LUCKY LTD.
      Query Match   5.9%;   Score 71;   DB 2;   Length 3010;
      Best Local Similarity 26.9%;   Pred. No. 7.8e+02;
RESULT 1120
ID   AAR53417 standard; protein; 3010 AA.
DE   Blood transmissible NANBHV protein.
PN   JP06105690-A.
PD   19-APR-1994.
PA   (KAEN/) KAENNO K.
      Query Match   5.9%;   Score 71;   DB 2;   Length 3010;
      Best Local Similarity 26.9%;   Pred. No. 7.8e+02;
RESULT 1121
ID   ABR83573 standard; protein; 202 AA.
DE   BcrC amino acid sequence SEQ ID NO:40.
PN   WO2003057708-A2.
PD   17-JUL-2003.
PA   (UYNE-) UNIV NEWCASTLE VENTURES LTD.
      Query Match   5.9%;   Score 70.5; DB 6;   Length 202;
      Best Local Similarity 26.5%;   Pred. No. 21;
RESULT 1122
ID   AAU01287 standard; protein; 218 AA.
DE   Brassica napus fatty acid desaturase, Fad3C, partial sequence.
PN   WO200125453-A2.
PD   12-APR-2001.
PA   (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
      Query Match   5.9%;   Score 70.5; DB 4;   Length 218;
      Best Local Similarity 29.3%;   Pred. No. 24;
RESULT 1123
ID   AAU97208 standard; protein; 228 AA.
DE   Portion of a wheat sugar transport protein encoded by wrein.pk0006.b4.
PN   US5383776-B1.
PD   07-MAY-2002.
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
      Query Match   5.9%;   Score 70.5; DB 5;   Length 228;
      Best Local Similarity 21.6%;   Pred. No. 25;
RESULT 1124
ID   ABU08333 standard; protein; 228 AA.
DE   Wheat sugar transport protein #3.
PN   US2002178468-A1.
PD   28-NOV-2002.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
      Query Match   5.9%;   Score 70.5; DB 6;   Length 228;
      Best Local Similarity 21.6%;   Pred. No. 25;
RESULT 1125
ID   ADG47920 standard; protein; 228 AA.
DE   Wheat Arabidopsis-like sugar transport protein #3.
PN   US2002199217-A1.
PD   26-DEC-2002.
PA   (HELE/) HELENTJARIS T G.
      Query Match   5.9%;   Score 70.5; DB 8;   Length 228;
      Best Local Similarity 21.6%;   Pred. No. 25;
RESULT 1126
ID   ABU17430 standard; protein; 275 AA.
DE   Protein encoded by Prokaryotic essential gene #2957.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   5.9%;   Score 70.5; DB 6;   Length 275;
      Best Local Similarity 22.8%;   Pred. No. 33;
RESULT 1127
ID   ABB55033 standard; protein; 285 AA.
DE   Lactococcus lactis protein malG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
      Query Match   5.9%;   Score 70.5; DB 5;   Length 285;
      Best Local Similarity 26.1%;   Pred. No. 34;
RESULT 1128
ID   ABB05467 standard; protein; 291 AA.
DE   Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.

PN   JP200132171-A.
PD   20-NOV-2001.
PA   (WARI/) WARIISHI H.
PA   (KUBI) KUBOTA CORP.
      Query Match   5.9%;   Score 70.5; DB 5;   Length 291;
      Best Local Similarity 29.4%;   Pred. No. 35;
RESULT 1129
ID   ADA35787 standard; protein; 297 AA.
DE   Acinetobacter baumannii protein #2948.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
      Query Match   5.9%;   Score 70.5; DB 6;   Length 297;
      Best Local Similarity 24.1%;   Pred. No. 36;
RESULT 1130
ID   ABM70358 standard; protein; 321 AA.
DE   Photorhabdus luminescens protein sequence #3455.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
      Query Match   5.9%;   Score 70.5; DB 6;   Length 321;
      Best Local Similarity 19.2%;   Pred. No. 40;
RESULT 1131
ID   ADH22355 standard; protein; 330 AA.
DE   Human receptor & membrane associated protein (REMAP) SeqID5.
PN   WO200310439S-A2.
PD   18-DEC-2003.
PA   (INCY-) INCYTE CORP.
      Query Match   5.9%;   Score 70.5; DB 8;   Length 330;
      Best Local Similarity 24.2%;   Pred. No. 42;
RESULT 1132
ID   ADK68232 standard; protein; 343 AA.
DE   Novel NOVX protein #79.
PN   WO200308S124-A2.
PD   16-OCT-2003.
PA   (CURA-) CURAGEN CORP.
      Query Match   5.9%;   Score 70.5; DB 7;   Length 343;
      Best Local Similarity 30.0%;   Pred. No. 44;
RESULT 1133
ID   ADH72226 standard; protein; 343 AA.
DE   Human protein of the invention NOV55a SEQ ID NO:1122.
PN   WO200310215S-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
      Query Match   5.9%;   Score 70.5; DB 8;   Length 343;
      Best Local Similarity 30.0%;   Pred. No. 44;
RESULT 1134
ID   ADR49221 standard; protein; 343 AA.
DE   Human NOV10a protein.
PN   US2004162236-A1.
PD   19-AUG-2004.
PA   (ALSO/) ALSOBROOK J.
PA   (BENT/) BENTO P.
PA   (BOLD/) BOLDOG F.
PA   (BURG/) BURGESS C.
PA   (CASM/) CASMAN S.
PA   (BOKO/) BOKOR J C.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (FERN/) FERNANDES B.
PA   (GERL/) GERLACH V.
PA   (GROS/) GROSSE W.
PA   (GUNT/) GUNTHER E.
PA   (GUSE/) GUSEV V.
PA   (HEYE/) HEYES M.
PA   (LEPL/) LEPLEY D.
PA   (LILL/) LI L.
PA   (MACD/) MACDOUGALL J R.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLET I.
PA   (PATT/) PATTURAJAN M.
PA   (PEYM/) PEYMAN J A.

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PA   (RAST/)  RASTELLI L.
PA   (RIEG/)  RIEGER D.
PA   (SHEN/)  SHENOY S.
PA   (SHIM/)  SHIMKETS R.
PA   (SMIT/)  SMITHSON G.
PA   (STON/)  STONE D.
PA   (VERN/)  VERNET C.
PA   (VOSS/)  VOSS E.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 343;
Best Local Similarity  30.0%;  Pred. No. 44;
RESULT 1135
ID   ADR40543 standard; protein; 363 AA.
DE   Ovine melatonin receptor O46608 protein.
PN   US2004161823-A1.
PD   19-AUG-2004.
PA   (FEDE/)  FEDER J N.
PA   (MINT/)  MINTIER G.
PA   (RAMA/)  RAMANATHAN C S.
PA   (HAWK/)  HAWKEN D R.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 363;
Best Local Similarity  23.1%;  Pred. No. 48;
RESULT 1136
ID   AAR69518 standard; protein; 365 AA.
DE   Prostaglandin-EP3-9 receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI )  MERCK FROSST CANADA INC.
Query Match             5.9%;  Score 70.5;  DB 2;  Length 365;
Best Local Similarity  24.2%;  Pred. No. 48;
RESULT 1137
ID   AAE38521 standard; protein; 365 AA.
DE   Human PTGER3 protein isoform, EP3b.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-)  DECODE GENETICS EHF.
Query Match             5.9%;  Score 70.5;  DB 7;  Length 365;
Best Local Similarity  24.2%;  Pred. No. 48;
RESULT 1138
ID   ADI35077 standard; protein; 365 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-)  DECODE GENETICS EHF.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 365;
Best Local Similarity  24.2%;  Pred. No. 48;
RESULT 1139
ID   ADL15889 standard; protein; 365 AA.
DE   Human prostaglandin E2 EP3 III.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR )  ALLERGAN INC.
PA   (UYAR-)  UNIV ARIZONA.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 365;
Best Local Similarity  24.2%;  Pred. No. 48;
RESULT 1140
ID   ADR67864 standard; protein; 365 AA.
DE   Prostaglandin E2 EP3 III.
PN   WO2004074830-A2.
PD   02-SEP-2004.
PA   (FARB )  BAYER HEALTHCARE AG.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 365;
Best Local Similarity  24.2%;  Pred. No. 48;
RESULT 1141
ID   ADS21429 standard; protein; 366 AA.
DE   Bacterial polypeptide #10462.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/)  CAO Y.
PA   (HINK/)  HINKLE G J.
PA   (SLAT/)  SLATER S C.
PA   (CHEN/)  CHEN X.
PA   (GOLD/)  GOLDMAN B S.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 366;

Best Local Similarity  21.2%;  Pred. No. 48;
RESULT 1142
ID   ADF04358 standard; protein; 367 AA.
DE   Bacterial polypeptide #471.
PN   US6605709-B1.
PD   12-AUG-2003.
PA   (GENO-)  GENOME THERAPEUTICS CORP.
Query Match             5.9%;  Score 70.5;  DB 7;  Length 367;
Best Local Similarity  33.3%;  Pred. No. 49;
RESULT 1143
ID   AAE38520 standard; protein; 374 AA.
DE   Human PTGER3 protein isoform, EP3d.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-)  DECODE GENETICS EHF.
Query Match             5.9%;  Score 70.5;  DB 7;  Length 374;
Best Local Similarity  24.2%;  Pred. No. 50;
RESULT 1144
ID   ADI35075 standard; protein; 374 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-)  DECODE GENETICS EHF.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 374;
Best Local Similarity  24.2%;  Pred. No. 50;
RESULT 1145
ID   AAR48711 standard; protein; 379 AA.
DE   G-protein coupled rat serotonin 2 receptor protein.
PN   WO9405695-A1.
PD   17-MAR-1994.
PA   (UYNY )  UNIV NEW YORK STATE.
Query Match             5.9%;  Score 70.5;  DB 2;  Length 379;
Best Local Similarity  22.9%;  Pred. No. 51;
RESULT 1146
ID   AAW02683 standard; peptide; 379 AA.
DE   G-protein coupled rat serotonin 2 receptor.
PN   US5508384-A.
PD   16-APR-1996.
PA   (UYNY )  UNIV NEW YORK STATE.
Query Match             5.9%;  Score 70.5;  DB 2;  Length 379;
Best Local Similarity  22.9%;  Pred. No. 51;
RESULT 1147
ID   AAR69517 standard; protein; 388 AA.
DE   Prostaglandin-EP3-21 receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI )  MERCK FROSST CANADA INC.
Query Match             5.9%;  Score 70.5;  DB 2;  Length 388;
Best Local Similarity  24.2%;  Pred. No. 52;
RESULT 1148
ID   AAE38513 standard; protein; 388 AA.
DE   Human PTGER3 protein isoform, EP3c.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-)  DECODE GENETICS EHF.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 388;
Best Local Similarity  24.2%;  Pred. No. 52;
RESULT 1149
ID   ADI35061 standard; protein; 388 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-)  DECODE GENETICS EHF.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 388;
Best Local Similarity  24.2%;  Pred. No. 52;
RESULT 1150
ID   ADL15887 standard; protein; 388 AA.
DE   Human prostaglandin EP3 receptor #2.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR )  ALLERGAN INC.
PA   (UYAR-)  UNIV ARIZONA.
Query Match             5.9%;  Score 70.5;  DB 8;  Length 388;
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  Best Local Similarity 24.2%;  Pred. No. 52;
RESULT 1151
ID   ADS13753 standard; protein; 388 AA.
DE   Human prostaglandin E2 EP3 II polypeptide.
PN   WO2004075813-A2.
PD   10-SEP-2004.
PA   (FARB ) BAYER HEALTHCARE AG.
  Query Match      5.9%;  Score 70.5;  DB 8;  Length 388;
  Best Local Similarity 24.2%;  Pred. No. 52;
RESULT 1152
ID   AAR69516 standard; protein; 390 AA.
DE   Prostaglandin-EP3-alpha receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MBRI ) MERCK FROSST CANADA INC.
  Query Match      5.9%;  Score 70.5;  DB 2;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1153
ID   AAE38516 standard; protein; 390 AA.
DE   Human PTGER3 protein isoform, EP3a1.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 7;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1154
ID   AAE38517 standard; protein; 390 AA.
DE   Human PTGER3 protein isoform, EP3a2.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 7;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1155
ID   ADI35067 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 8;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1156
ID   ADI35069 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 8;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1157
ID   ADL15898 standard; protein; 390 AA.
DE   Human prostaglandin EP3 receptor #4.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR ) ALLERGAN INC.
PA   (UYAR-) UNIV ARIZONA.
  Query Match      5.9%;  Score 70.5;  DB 8;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1158
ID   ADL15885 standard; protein; 390 AA.
DE   Human prostaglandin EP3 receptor #1.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLR ) ALLERGAN INC.
PA   (UYAR-) UNIV ARIZONA.
  Query Match      5.9%;  Score 70.5;  DB 8;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1159
ID   ADR70434 standard; protein; 390 AA.
DE   Human prostaglandin E2 EP3 protein.
PN   WO2004074842-A2.
PD   02-SEP-2004.
PA   (FARB ) BAYER HEALTHCARE AG.

  Query Match      5.9%;  Score 70.5;  DB 8;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1160.*
ID   ADS76168 standard; protein; 390 AA.
DE   Prostaglandin E2 EP3 I.
PN   WO2004075814-A2.
PD   10-SEP-2004.
PA   (FARB ) BAYER HEALTHCARE AG.
  Query Match      5.9%;  Score 70.5;  DB 8;  Length 390;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1161
ID   AAW57411 standard; protein; 393 AA.
DE   Human prostaglandin EP3-VI receptor.
PN   JP10113185-A.
PD   06-MAY-1998.
PA   (ONOY ) ONO PHARM CO LTD.
  Query Match      5.9%;  Score 70.5;  DB 2;  Length 393;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1162
ID   AAE38519 standard; protein; 393 AA.
DE   Human PTGER3 protein isoform, EP3e.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 7;  Length 393;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1163
ID   AAE38523 standard; protein; 393 AA.
DE   Human PTGER3 protein isoform, EP3-VI.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 7;  Length 393;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1164
ID   ADI35081 standard; protein; 393 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 8;  Length 393;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1165
ID   ADI35073 standard; protein; 393 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 8;  Length 393;
  Best Local Similarity 24.2%;  Pred. No. 53;
RESULT 1166
ID   AAW57410 standard; protein; 402 AA.
DE   Human EP3-V receptor.
PN   JP10113185-A.
PD   06-MAY-1998.
PA   (ONOY ) ONO PHARM CO LTD.
  Query Match      5.9%;  Score 70.5;  DB 2;  Length 402;
  Best Local Similarity 24.2%;  Pred. No. 55;
RESULT 1167
ID   ABP81904 standard; protein; 402 AA.
DE   Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN   WO2002061087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
  Query Match      5.9%;  Score 70.5;  DB 6;  Length 402;
  Best Local Similarity 24.2%;  Pred. No. 55;
RESULT 1168
ID   AAE38522 standard; protein; 402 AA.
DE   Human PTGER3 protein isoform, EP3-V.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match      5.9%;  Score 70.5;  DB 7;  Length 402;
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     Best Local Similarity   24.2%;   Pred. No. 55;
RESULT 1169
ID   ADI35079 standard; protein; 402 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 402;
     Best Local Similarity   24.2%;   Pred. No. 55;
RESULT 1170
ID   ADO55167 standard; protein; 402 AA.
DE   Protein #69 with increased gene expression in renal cell carcinoma.
PN   WO2004032842-A2.
PD   22-APR-2004.
PA   (VAND-) VAN ANDEL INST.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 402;
     Best Local Similarity   24.2%;   Pred. No. 55;
RESULT 1171
ID   ADO29620 standard; protein; 402 AA.
DE   Human GPCR PTGER3, SEQ ID NO:722.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 402;
     Best Local Similarity   24.2%;   Pred. No. 55;
RESULT 1172
ID   AAE38514 standard; protein; 407 AA.
DE   Human PTGER3 protein isoform, EP3g.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 7;  Length 407;
     Best Local Similarity   24.2%;   Pred. No. 56;
RESULT 1173
ID   ADI35063 standard; protein; 407 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 407;
     Best Local Similarity   24.2%;   Pred. No. 56;
RESULT 1174
ID   AAE38518 standard; protein; 425 AA.
DE   Human PTGER3 protein isoform, EP3f.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 7;  Length 425;
     Best Local Similarity   24.2%;   Pred. No. 59;
RESULT 1175
ID   ADI35071 standard; protein; 425 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 425;
     Best Local Similarity   24.2%;   Pred. No. 59;
RESULT 1176
ID   AAE38515 standard; protein; 433 AA.
DE   Human PTGER3 protein isoform, EP3h.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 7;  Length 433;
     Best Local Similarity   24.2%;   Pred. No. 61;
RESULT 1177
ID   ADI35065 standard; protein; 433 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 433;
     Best Local Similarity   24.2%;   Pred. No. 61;
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RESULT 1178
ID   AAW98431 standard; protein; 480 protein.
DE   H. pylori GHPO 446 protein.
PN   WO9841478-A1.
PD   08-OCT-1998.
PA   (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             5.9%;   Score 70.5;  DB 2;  Length 480;
     Best Local Similarity   23.1%;   Pred. No. 70;
RESULT 1179
ID   ABP40525 standard; protein; 499 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match             5.9%;   Score 70.5;  DB 5;  Length 499;
     Best Local Similarity   20.5%;   Pred. No. 74;
RESULT 1180
ID   ADS06092 standard; protein; 499 AA.
DE   Staphylococcus epidermis polypeptide seqid 5387.
PN   US2004147734-A1.
PD   29-JUL-2004.
PA   (DOUC/) DOUCETTE-STAMM L.
PA   (BUSH/) BUSH D.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 499;
     Best Local Similarity   20.5%;   Pred. No. 74;
RESULT 1181
ID   ABU30473 standard; protein; 521 AA.
DE   Protein encoded by Prokaryotic essential gene #16000.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             5.9%;   Score 70.5;  DB 6;  Length 521;
     Best Local Similarity   23.7%;   Pred. No. 79;
RESULT 1182
ID   AAU97213 standard; protein; 539 AA.
DE   Wheat sugar transport protein encoded by wlk8.pk0001.all.
PN   US6383776-B1.
PD   07-MAY-2002.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
     Query Match             5.9%;   Score 70.5;  DB 5;  Length 539;
     Best Local Similarity   26.0%;   Pred. No. 83;
RESULT 1183
ID   ABU08338 standard; protein; 539 AA.
DE   Wheat sugar transport protein #4.
PN   US2002178468-A1.
PD   28-NOV-2002.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
     Query Match             5.9%;   Score 70.5;  DB 6;  Length 539;
     Best Local Similarity   26.0%;   Pred. No. 83;
RESULT 1184
ID   ADG47930 standard; protein; 539 AA.
DE   Wheat Beta-vulgaris-like sugar transport protein #1.
PN   US2002199217-A1.
PD   26-DEC-2002.
PA   (HELB/) HELENTJARIS T G.
     Query Match             5.9%;   Score 70.5;  DB 8;  Length 539;
     Best Local Similarity   26.0%;   Pred. No. 83;
RESULT 1185
ID   ABU27418 standard; protein; 548 AA.
DE   Protein encoded by Prokaryotic essential gene #12945.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             5.9%;   Score 70.5;  DB 6;  Length 548;
     Best Local Similarity   24.0%;   Pred. No. 85;
RESULT 1186
ID   ADN22789 standard; protein; 556 AA.
DE   Bacterial polypeptide #5442.
PN   US2003233675-A1.
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PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match      5.9%;  Score 70.5;  DB 8;  Length 556
     Best Local Similarity  21.1%;  Pred. No. 86;
RESULT 1187
ID   ADD46023 standard; protein; 599 AA.
DE   Rat Protein P23978, SEQ ID NO 11695.
PN   WO200316475-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match      5.9%;  Score 70.5;  DB 7;  Length 599;
     Best Local Similarity  20.1%;  Pred. No. 96;
RESULT 1188
ID   ABW02687 standard; protein; 599 AA.
DE   Rattus norvegicus neuronal GABA transporter (GAT-1).
PN   US2003143729-A1.
PD   31-JUL-2003.
PA   (SYNA-) SYNAPTIC PHARM CORP.
     Query Match      5.9%;  Score 70.5;  DB 7;  Length 599;
     Best Local Similarity  20.1%;  Pred. No. 96;
RESULT 1189
ID   AAM78767 standard; protein; 600 AA.
DE   Human protein SEQ ID NO 1429.
PN   WO200157190-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match      5.9%;  Score 70.5;  DB 4;  Length 600;
     Best Local Similarity  19.5%;  Pred. No. 96;
RESULT 1190
ID   ADJ64315 standard; protein; 662 AA.
DE   Cartilage differentiation inhibiting protein, SEQ ID 10.
PN   WO2004011326-A1.
PD   12-FEB-2004.
PA   (ASAH ) ASAHI KASEI KK.
     Query Match      5.9%;  Score 70.5;  DB 8;  Length 662;
     Best Local Similarity  22.7%;  Pred. No. 1.1e+02;
RESULT 1191
ID   ABB92892 standard; protein; 700 AA.
DE   Herbicidally active polypeptide SEQ ID NO 2103.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB ) BAYER AG.
     Query Match      5.9%;  Score 70.5;  DB 5;  Length 700;
     Best Local Similarity  25.8%;  Pred. No. 1.2e+02;
RESULT 1192
ID   AAB56721 standard; protein; 717 AA.
DE   Human prostate cancer antigen protein sequence SEQ ID NO:1299.
PN   WO200055174-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
     Query Match      5.9%;  Score 70.5;  DB 3;  Length 717;
     Best Local Similarity  22.4%;  Pred. No. 1.2e+02;
RESULT 1193
ID   ADG47941 standard; protein; 740 AA.
DE   Arabidopsis thaliana-like sugar transport protein #2.
PN   US200219217-A1.
PD   26-DEC-2002.
PA   (HELE/) HELENTJARIS T G.
     Query Match      5.9%;  Score 70.5;  DB 8;  Length 740;
     Best Local Similarity  22.8%;  Pred. No. 1.3e+02;
RESULT 1194
ID   AAG39555 standard; protein; 766 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match      5.9%;  Score 70.5;  DB 3;  Length 766;
     Best Local Similarity  21.3%;  Pred. No. 1.3e+02;

RESULT 1195
ID   AAG39554 standard; protein; 815 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match      5.9%;  Score 70.5;  DB 3;  Length 815;
     Best Local Similarity  21.3%;  Pred. No. 1.5e+02;
RESULT 1196
ID   AAG39553 standard; protein; 927 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match      5.9%;  Score 70.5;  DB 3;  Length 927;
     Best Local Similarity  21.3%;  Pred. No. 1.8e+02;
RESULT 1197
ID   ABP73754 standard; protein; 1026 AA.
DE   Candida albicans essential protein SEQ ID NO 7591.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match      5.9%;  Score 70.5;  DB 5;  Length 1026;
     Best Local Similarity  22.3%;  Pred. No. 2e+02;
RESULT 1198
ID   AAW17057 standard; protein; 1027 AA.
DE   Candida albicans chitin synthae (CHS1).
PN   WO9716540-A1.
PD   09-MAY-1997.
PA   (CHEM-) CHEMGENICS PHARM INC.
     Query Match      5.9%;  Score 70.5;  DB 2;  Length 1027;
     Best Local Similarity  22.3%;  Pred. No. 2e+02;
RESULT 1199
ID   ADH22510 standard; protein; 1147 AA.
DE   Human transporter & ion channel (TRICH) protein SeqID8.
PN   WO2003093444-A2.
PD   13-NOV-2003.
PA   (INCY-) INCYTE CORP.
     Query Match      5.9%;  Score 70.5;  DB 8;  Length 1147;
     Best Local Similarity  19.5%;  Pred. No. 2.4e+02;
RESULT 1200
ID   ADK18350 standard; protein; 1163 AA.
DE   Human NOVX protein #2.
PN   WO2003057854-A2.
PD   17-JUL-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match      5.9%;  Score 70.5;  DB 7;  Length 1163;
     Best Local Similarity  19.5%;  Pred. No. 2.4e+02;
RESULT 1201
ID   ADM29274 standard; protein; 1163 AA.
DE   Human novel protein NOV2b.
PN   WO2003064628-A2.
PD   07-AUG-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match      5.9%;  Score 70.5;  DB 7;  Length 1163;
     Best Local Similarity  19.5%;  Pred. No. 2.4e+02;
RESULT 1202
ID   AAW53863 standard; peptide; 1780 AA.
DE   Human gravin polypeptide.
PN   US5741890-A.
PD   21-APR-1998.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match      5.9%;  Score 70.5;  DB 2;  Length 1780;
     Best Local Similarity  34.8%;  Pred. No. 4.3e+02;
RESULT 1203
ID   AAB15380 standard; protein; 1780 AA.
DE   Human gravin protein sequence.
PN   US6090929-A.
PD   18-JUL-2000.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match      5.9%;  Score 70.5;  DB 3;  Length 1780;
     Best Local Similarity  34.8%;  Pred. No. 4.3e+02;
RESULT 1204
ID   AAO17365 standard; protein; 1781 AA.
DE   Human gravin.
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PN   EP1191107-A2.
PD   27-MAR-2002.
PA   (SCHD) SCHERING AG.
  Query Match   5.9%; Score 70.5; DB 5; Length 1781;
  Best Local Similarity 34.8%; Pred. No. 4.3e+02;
RESULT 1205
ID   ABU03477 standard; protein; 1781 AA.
DE   Angiogenesis-associated human protein sequence #22.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match   5.9%; Score 70.5; DB 6; Length 1781;
  Best Local Similarity 34.8%; Pred. No. 4.3e+02;
RESULT 1206
DE   Novel human protein SEQ ID NO: 716.
PN   WO200222660-A2.
PD   21-MAR-2002.
PA   (HYSE-) HYSEQ INC.
  Query Match   5.9%; Score 70.5; DB 5; Length 1783;
  Best Local Similarity 34.8%; Pred. No. 4.3e+02;
RESULT 1207
ID   ABG21018 standard; protein; 1795 AA.
DE   Novel human diagnostic protein #21009.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match   5.9%; Score 70.5; DB 4; Length 1795;
  Best Local Similarity 34.8%; Pred. No. 4.4e+02;
RESULT 1208
ID   AAG34242 standard; protein; 185 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match   5.9%; Score 70; DB 3; Length 185;
  Best Local Similarity 26.2%; Pred. No. 21;
RESULT 1209
ID   AAG34241 standard; protein; 189 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41630.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match   5.9%; Score 70; DB 3; Length 189;
  Best Local Similarity 26.2%; Pred. No. 22;
RESULT 1210
ID   AAM44944 standard; protein; 225 AA.
DE   Avian infectious bronchitis virus glycoprotein M.
PN   FR2751225-A1.
PD   23-JAN-1998.
PA   (INMR) RHONE MERIEUX SA.
  Query Match   5.9%; Score 70; DB 2; Length 225;
  Best Local Similarity 21.6%; Pred. No. 28;
RESULT 1211
ID   ADB09893 standard; protein; 226 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:3730.
PN   WO200304304-A2.
PD   12-JUN-2003.
PA   (AMHP) WYETH HOLDINGS CORP.
  Query Match   5.9%; Score 70; DB 6; Length 226;
  Best Local Similarity 24.1%; Pred. No. 28;
RESULT 1212
ID   AAG34240 standard; protein; 235 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41629.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match   5.9%; Score 70; DB 3; Length 235;
  Best Local Similarity 26.2%; Pred. No. 30;
RESULT 1213
ID   ABB69790 standard; protein; 256 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 36162.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PBKE) PE CORP NY.
  Query Match   5.9%; Score 70; DB 4; Length 256;

  Best Local Similarity 20.2%; Pred. No. 34;
RESULT 1214
ID   ADS96502 standard; protein; 256 AA.
DE   Drosophila melanogaster protein, SEQ ID 123.
PN   WO200403999-A2.
PD   13-MAY-2004.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
  Query Match   5.9%; Score 70; DB 8; Length 256;
  Best Local Similarity 20.2%; Pred. No. 34;
RESULT 1215
ID   ADT05703 standard; protein; 256 AA.
DE   Haemophilus influenzae (NTHi) protein - SEQ ID 739.
PN   WO2004078949-A2.
PD   16-SEP-2004.
PA   (CHIL-) CHILDRENS HOSPITAL INC.
  Query Match   5.9%; Score 70; DB 8; Length 256;
  Best Local Similarity 18.3%; Pred. No. 34;
RESULT 1216
ID   AAG53762 standard; protein; 274 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68478.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match   5.9%; Score 70; DB 3; Length 274;
  Best Local Similarity 26.0%; Pred. No. 37;
RESULT 1217
ID   AAG53761 standard; protein; 287 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68477.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match   5.9%; Score 70; DB 3; Length 287;
  Best Local Similarity 26.0%; Pred. No. 40;
RESULT 1218
ID   ABU35677 standard; protein; 292 AA.
DE   Protein encoded by Prokaryotic essential gene #21204.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match   5.9%; Score 70; DB 6; Length 292;
  Best Local Similarity 22.5%; Pred. No. 40;
RESULT 1219
ID   ADK48488 standard; protein; 307 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 5003.
PN   US6699703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   5.9%; Score 70; DB 8; Length 307;
  Best Local Similarity 26.2%; Pred. No. 43;
RESULT 1220
ID   AAR72985 standard; protein; 333 AA.
DE   Epsilon opioid receptor.
PN   WO9512670-A1.
PD   11-MAY-1995.
PA   (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.
  Query Match   5.9%; Score 70; DB 2; Length 333;
  Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1221
ID   AAY90613 standard; protein; 333 AA.
DE   Human G protein-coupled receptor GPR8.
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
  Query Match   5.9%; Score 70; DB 3; Length 333;
  Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1222
ID   AAY90647 standard; protein; 333 AA.
DE   Human mutant G protein-coupled receptor GPR8 (T259K).
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
  Query Match   5.9%; Score 70; DB 3; Length 333;
  Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1223
ID   AAU01297 standard; protein; 333 AA.

DE   Human G-protein receptor 8, GPR 8, mutant N127A.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K M.
     Query Match   5.9%; Score 70; DB 4; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1224
ID   AAU01295 standard; protein; 333 AA.
DE   Human G-protein receptor 8, GPR 8.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K M.
RESULT 1225
     Query Match   5.9%; Score 70; DB 4; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
ID   AAU01298 standard; protein; 333 AA.
DE   Human G-protein receptor 8, GPR 8, mutant T259E.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
PA   (WILL/) WILLIAMS K M.
RESULT 1226
     Query Match   5.9%; Score 70; DB 4; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
ID   ABB84683 standard; protein; 333 AA.
DE   Human GPR8-ligand related protein #1.
PN   WO200198494-A1.
PD   27-DEC-2001.
PA   (TAKE) TAKEDA CHEM IND LTD.
RESULT 1227
     Query Match   5.9%; Score 70; DB 5; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
ID   ABB84723 standard; protein; 333 AA.
DE   Human GPR8-ligand related protein #3.
PN   WO200198494-A1.
PD   27-DEC-2001.
PA   (TAKE) TAKEDA CHEM IND LTD.
RESULT 1228
     Query Match   5.9%; Score 70; DB 5; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
ID   ABG65918 standard; protein; 333 AA.
DE   G protein-coupled receptor related peptide #6.
PN   WO200291161-A1.
PD   21-NOV-2002.
PA   (TAKE) TAKEDA CHEM IND LTD.
RESULT 1229
     Query Match   5.9%; Score 70; DB 5; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
ID   ABU61448 standard; protein; 333 AA.
DE   Screening method related protein #1.
PN   WO200293161-A1.
PD   06-JUN-2002.
PA   (TAKE) TAKEDA CHEM IND LTD.
RESULT 1230
     Query Match   5.9%; Score 70; DB 6; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
ID   ABJ37874 standard; protein; 333 AA.
DE   GPR7 ligand related human protein SEQ ID No 84.
PN   WO200210847-A1.
PD   27-DEC-2002.
PA   (TAKE) TAKEDA CHEM IND LTD.
RESULT 1231
     Query Match   5.9%; Score 70; DB 6; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
ID   ABP81897 standard; protein; 333 AA.
DE   Human G protein-coupled receptor GPR8 protein SEQ ID NO:279.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   5.9%; Score 70; DB 6; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;

RESULT 1232
ID   ABR57245 standard; protein; 333 AA.
DE   Human GPR8 protein SEQ ID NO:84.
PN   WO2003045994-A1.
PD   05-JUN-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1233
ID   ADC22691 standard; protein; 333 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #44.
PN   US6655339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1234
ID   ADC22535 standard; protein; 333 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #5.
PN   US6655339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1235
ID   ADC51793 standard; protein; 333 AA.
DE   Human GPR8, SEQ ID 4.
PN   WO2003057236-A1.
PD   17-JUL-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1236
ID   ABR61545 standard; protein; 333 AA.
DE   Human GPR8 receptor polypeptide.
PN   WO2003081234-A2.
PD   02-OCT-2003.
PA   (FARB-) BAYER AG.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1237
ID   ADG41976 standard; protein; 333 AA.
DE   Human GPR8 polypeptide.
PN   JP2003009867-A.
PD   14-JAN-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1238
ID   ADH14008 standard; protein; 333 AA.
DE   Human GPR8.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1239
ID   ADH14164 standard; protein; 333 AA.
DE   Mutated human GPR8.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match   5.9%; Score 70; DB 7; Length 333;
     Best Local Similarity   23.6%; Pred. No. 49;
RESULT 1240
ID   ADG12852 standard; protein; 333 AA.
DE   Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
PN   WO2003097795-A2.
PD   27-NOV-2003.

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PA    (NORA-) NORAK BIOSCI INC.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 49;
RESULT 1241
ID    ADO29700 standard; protein; 333 AA.                          Length 333;
DB    Human GPCR GPR8, SEQ ID NO:802.
PN    WO2004040000-A2.
PD    13-MAY-2004.
PA    (PRIM-) PRIMAL INC.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 49;
RESULT 1242
ID    ADO31044 standard; protein; 333 AA.                          Length 333;
DB    Human GPR8 protein SEQ ID NO:73.
PN    WO2004041301-A1.
PD    21-MAY-2004.
PA    (TAKE ) TAKEDA CHEM IND LTD.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 49;
RESULT 1243
ID    ADQ19919 standard; protein; 333 AA.                          Length 333;
DE    Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.
PN    WO2004048938-A2.
PD    10-JUN-2004.
PA    (PROT-) PROTEIN DESIGN LABS INC.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 49;
RESULT 1244
ID    ADS14162 standard; protein; 333 AA.                          Length 333;
DE    Human GPR8 ligand protein SeqID 73.
PN    WO2004080485-A1.
PD    23-SEP-2004.
PA    (TAKE ) TAKEDA CHEM IND LTD.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 49;
RESULT 1245
ID    ADG12854 standard; protein; 347 AA.                          Length 347;
DE    Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
PN    WO2003097795-A2.
PD    27-NOV-2003.
PA    (NORA-) NORAK BIOSCI INC.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 51;
RESULT 1246
ID    ABG30839 standard; protein; 364 AA.                          Length 364;
DE    Human calcium channel protein.
PN    WO200252003-A2.
PD    04-JUL-2002.
PA    (FARB ) BAYER AG.
      Query Match           5.9%;      Score 70;    DB 5;
      Best Local Similarity 25.0%;     Pred. No. 55;
RESULT 1247
ID    ADG12856 standard; protein; 364 AA.                          Length 364;
DE    Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
PN    WO2003097795-A2.
PD    27-NOV-2003.
PA    (NORA-) NORAK BIOSCI INC.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 55;
RESULT 1248
ID    ADC28778 standard; protein; 364 AA.                          Length 364;
DE    Human GPR8-enhanced receptor.
PN    US2004091946-A1.
PD    13-MAY-2004.
PA    (OAKL/) OAKLEY R H.
PA    (BARA/) BARAK L S.
PA    (LAPO/) LAPORTE S A.
PA    (CARO/) CARON M G.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 55;
RESULT 1249
ID    ADG12858 standard; protein; 378 AA.                          Length 378;
DE    HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.

PN    WO2003097795-A2.
PD    27-NOV-2003.
PA    (NORA-) NORAK BIOSCI INC.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 23.6%;     Pred. No. 58;
RESULT 1250
ID    ADN49121 standard; protein; 388 AA.                          Length 378;
DE    Mouse oxytocin receptor protein.
PN    US2004086881-A1.
PD    06-MAY-2004.
PA    (RAMA/) RAMANATHAN C S.
PA    (GOPA/) GOPAL S.
PA    (MINT/) MINTIER G A.
PA    (FEDE/) FEDER J.
      Query Match           5.9%;      Score 70;    DB 8;    Length 388;
      Best Local Similarity 24.8%;     Pred. No. 60;
RESULT 1251
ID    ADO29591 standard; protein; 388 AA.                          Length 388;
DE    Mouse GPCR OXTR, SEQ ID NO:693.
PN    WO2004040000-A2.
PD    13-MAY-2004.
PA    (PRIM-) PRIMAL INC.
      Query Match           5.9%;      Score 70;    DB 8;
      Best Local Similarity 24.8%;     Pred. No. 60;
RESULT 1252
ID    ADA54410 standard; protein; 399 AA.                          Length 388;
DE    Human protein, SEQ ID 1978.
PN    EP1293569-A2.
PD    19-MAR-2003.
PA    (HELI-) HELIX RES INST.
PA    (REAS-) RES ASSOC BIOTECHNOLOGY.
      Query Match           5.9%;      Score 70;    DB 6;    Length 399;
      Best Local Similarity 22.9%;     Pred. No. 62;
RESULT 1253
ID    ABG99947 standard; protein; 399 AA.                          Length 399;
DE    Human novel polypeptide #60.
PN    WO200274961-A1.
PD    26-SEP-2002.
PA    (HYSB-) HYSEQ INC.
      Query Match           5.9%;      Score 70;    DB 6;    Length 399;
      Best Local Similarity 22.9%;     Pred. No. 62;
RESULT 1254
ID    ADC96947 standard; protein; 425 AA.
DE    E. faecium protein sequence SEQ ID 6574.
PN    US6583275-B1.
PD    24-JUN-2003.
PA    (GENO-) GENOME THERAPEUTICS CORP.
      Query Match           5.9%;      Score 70;    DB 7;    Length 425;
      Best Local Similarity 25.9%;     Pred. No. 68;
RESULT 1255
ID    ADA34110 standard; protein; 470 AA.
DE    Acinetobacter baumannii protein #1271.
PN    US6552958-B1.
PD    13-MAY-2003.
PA    (GENO-) GENOME THERAPEUTICS CORP.
      Query Match           5.9%;      Score 70;    DB 6;    Length 470;
      Best Local Similarity 23.5%;     Pred. No. 78;
RESULT 1256
ID    ABM67264 standard; protein; 474 AA.
DE    Photorhabdus luminescens protein sequence #361.
PN    WO200294867-A2.
PD    28-NOV-2002.
PA    (INSP ) INST PASTEUR.
PA    (CNRS ) CNRS CENT NAT RECH SCI.
      Query Match           5.9%;      Score 70;    DB 6;    Length 474;
      Best Local Similarity 22.9%;     Pred. No. 79;
RESULT 1257
ID    AAB16787 standard; protein; 475 AA.
DE    Human transporter and ion channel-24 (TRICH-24) protein.
PN    WO20019304-A2.
PD    06-DEC-2001.
PA    (INCY-) INCYTE GENOMICS INC.
      Query Match           5.9%;      Score 70;    DB 5;    Length 475;
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      Best Local Similarity   25.0%;   Pred. No. 79;
RESULT 1258
ID   ADA89683 standard; protein; 506 AA.
DE   Staphylococcus aureus antigenic protein #222.
PN   WO200301899-A2.
PD   13-FEB-2003.
PA   (UYSH-) UNIV SHEFFIELD.
PA   (BIOS-) BIOSYNEXUS INC.
      Query Match            5.9%;   Score 70;   DB 6;   Length 506;
      Best Local Similarity   20.1%;   Pred. No. 87;
RESULT 1259
ID   ABM72414 standard; protein; 506 AA.
DE   Staphylococcus aureus protein #1654.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
      Query Match            5.9%;   Score 70;   DB 6;   Length 506;
      Best Local Similarity   20.1%;   Pred. No. 87;
RESULT 1260
ID   AAE21176 standard; protein; 540 AA.
DE   Human TRICH-20 protein.
PN   WO200212340-A2.
PD   14-FEB-2002.
PA   (INCY-) INCYTE GENOMICS INC.
      Query Match            5.9%;   Score 70;   DB 5;   Length 540;
      Best Local Similarity   25.0%;   Pred. No. 95;
RESULT 1261
ID   AAM39017 standard; protein; 552 AA.
DE   Human polypeptide SEQ ID NO 2162.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
      Query Match            5.9%;   Score 70;   DB 4;   Length 552;
      Best Local Similarity   25.0%;   Pred. No. 98;
RESULT 1262
ID   ABU18262 standard; protein; 602 AA.
DE   Protein encoded by Prokaryotic essential gene #3789.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match            5.9%;   Score 70;   DB 6;   Length 602;
      Best Local Similarity   26.4%;   Pred. No. 1.1e+02;
RESULT 1263
ID   ABU33453 standard; protein; 637 AA.
DE   Protein encoded by Prokaryotic essential gene #18980.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match            5.9%;   Score 70;   DB 6;   Length 637;
      Best Local Similarity   23.1%;   Pred. No. 1.2e+02;
RESULT 1264
ID   AAY91335 standard; protein; 640 AA.
DE   Group B Streptococcus protein sequence SEQ ID NO:68.
PN   WO200006736-A2.
PD   10-FEB-2000.
PA   (MICR-) MICROBIAL TECHNICS LTD.
      Query Match            5.9%;   Score 70;   DB 3;   Length 640;
      Best Local Similarity   21.4%;   Pred. No. 1.2e+02;
RESULT 1265
ID   ABM83818 standard; protein; 695 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:4067.
PN   WO200403973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
      Query Match            5.9%;   Score 70;   DB 8;   Length 695;
      Best Local Similarity   28.6%;   Pred. No. 1.3e+02;
RESULT 1266
ID   ADL04660 standard; protein; 767 AA.
DE   M. catarrhalis protein #426.
PN   US5673910-B1.
PD   06-JAN-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
      Query Match            5.9%;   Score 70;   DB 8;   Length 767;
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      Best Local Similarity   21.3%;   Pred. No. 1.5e+02;
RESULT 1267
ID   AAR53921 standard; protein; 980 AA.
DE   HCV fusion protein corresp. to N-terminal of ORF.
PN   JP06092996-A.
PD   05-APR-1994.
PA   (SHIM/) SHIMOTOYA K.
      Query Match            5.9%;   Score 70;   DB 2;   Length 980;
      Best Local Similarity   24.6%;   Pred. No. 2.2e+02;
RESULT 1268
ID   ADS24062 standard; protein; 1041 AA.
DE   Bacterial polypeptide #13095.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
      Query Match            5.9%;   Score 70;   DB 8;   Length 1041;
      Best Local Similarity   23.4%;   Pred. No. 2.4e+02;
RESULT 1269
ID   ADP07803 standard; protein; 138 AA.
DE   Human secreted protein, seq id 286.
PN   WO200404200-A2.
PD   21-MAY-2004.
PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match            5.9%;   Score 69.5;   DB 8;   Length 138;
      Best Local Similarity   22.0%;   Pred. No. 16;
RESULT 1270
ID   ADA33664 standard; protein; 198 AA.
DE   Acinetobacter baumannii protein #825.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
      Query Match            5.8%;   Score 69.5;   DB 6;   Length 198;
      Best Local Similarity   23.3%;   Pred. No. 27;
RESULT 1271
ID   ADB09276 standard; protein; 201 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:3216.
PN   WO200304304-A2.
PD   12-JUN-2003.
PA   (AMHP ) WYETH HOLDINGS CORP.
      Query Match            5.8%;   Score 69.5;   DB 6;   Length 201;
      Best Local Similarity   26.0%;   Pred. No. 28;
RESULT 1272
ID   AAU29449 standard; protein; 210 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #70.
PN   WO200168858-A2.
PD   20-SEP-2001.
PA   (PHAA ) PHARMACIA & UPJOHN CO.
      Query Match            5.8%;   Score 69.5;   DB 4;   Length 210;
      Best Local Similarity   20.9%;   Pred. No. 29;
RESULT 1273
ID   ABG60737 standard; protein; 210 AA.
DE   Novel G protein coupled receptor (nGCPR-x) #70.
PN   US2002058306-A1.
PD   16-MAY-2002.
PA   (VOGE/) VOGELI G.
      Query Match            5.8%;   Score 69.5;   DB 5;   Length 210;
      Best Local Similarity   20.9%;   Pred. No. 29;
RESULT 1274
ID   AAU01288 standard; protein; 218 AA.
DE   Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.
PN   WO200125453-A2.
PD   12-APR-2001.
PA   (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.
      Query Match            5.8%;   Score 69.5;   DB 4;   Length 218;
      Best Local Similarity   29.3%;   Pred. No. 31;
RESULT 1275
ID   ADB09278 standard; protein; 247 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:3218.
PN   WO200304304-A2.
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PD   12-JUN-2003.
PA   (AMHP) WYETH HOLDINGS CORP.
 Query Match   5.8%; Score 69.5; DB 6; Length 247;
  Best Local Similarity 26.0%; Pred. No. 37;
RESULT 1276
ID   ABG66935 standard; protein; 253 AA.
DE   Novel G-protein coupled receptor related protein #12.
PN   WO200240539-A2.
PD   23-MAY-2002.
PA   (CURA-) CURAGEN CORP.
 Query Match   5.8%; Score 69.5; DB 5; Length 253;
  Best Local Similarity 24.2%; Pred. No. 38;
RESULT 1277
ID   ABB62542 standard; protein; 261 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 14418.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
 Query Match   5.8%; Score 69.5; DB 5; Length 261;
  Best Local Similarity 27.7%; Pred. No. 40;
RESULT 1278
ID   ABO80446 standard; protein; 270 AA.
DE   Pseudomonas aeruginosa polypeptide #12621.
PN   US6651795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
 Query Match   5.8%; Score 69.5; DB 7; Length 270;
  Best Local Similarity 22.1%; Pred. No. 42;
RESULT 1279
ID   ADE86076 standard; protein; 296 AA.
DE   Streptomyces hygroscopicus ABC transporter.
PN   WO2003082909-A1.
PD   09-OCT-2003.
PA   (AMHP) WYETH.
 Query Match   5.8%; Score 69.5; DB 7; Length 296;
  Best Local Similarity 21.0%; Pred. No. 47;
RESULT 1280
ID   AAG71524 standard; protein; 308 AA.
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1205.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
 Query Match   5.8%; Score 69.5; DB 4; Length 308;
  Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1281
ID   ABB44525 standard; protein; 308 AA.
DE   Human GPCR3 polypeptide SEQ ID NO 9.
PN   WO200174904-A2.
PD   11-OCT-2001.
PA   (CURA-) CURAGEN CORP.
 Query Match   5.8%; Score 69.5; DB 4; Length 308;
  Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1282
ID   AAU24742 standard; protein; 308 AA.
DE   Human olfactory receptor AOLFR242.
PN   WO200168805-A2.
PD   20-SEP-2001.
PA   (SENO-) SENOMYX INC.
 Query Match   5.8%; Score 69.5; DB 4; Length 308;
  Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1283
ID   ABP95703 standard; protein; 308 AA.
DE   Human GPCR polypeptide SEQ ID NO 216.
PN   WO200216548-A2.
PD   28-FEB-2002.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match   5.8%; Score 69.5; DB 5; Length 308;
  Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1284
ID   AAU95729 standard; protein; 308 AA.
DE   Human olfactory and pheromone G protein-coupled receptor #216.
PN   WO200224726-A2.

PD   12-JUN-2003.
PA   (AMHP) ...

PD   28-MAR-2002.
PA   (CHEM-) CHEMCOM SA.
 Query Match   5.8%; Score 69.5; DB 5; Length 308;
  Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1285
ID   AAU85362 standard; protein; 308 AA.
DE   G-coupled olfactory receptor #223.
PN   WO200198526-A2.
PD   27-DEC-2001.
PA   (SENO-) SENOMYX INC.
 Query Match   5.8%; Score 69.5; DB 5; Length 308;
  Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1286
ID   ADC86333 standard; protein; 308 AA.
DE   Human GPCR protein SEQ ID NO:786.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match   5.8%; Score 69.5; DB 7; Length 308;
  Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1287
ID   ABW02126 standard; protein; 308 AA.
DE   Human GPCR3 protein.
PN   US2003195335-A1.
PD   16-OCT-2003.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERRES B S.
PA   (CASM/) CASMAN S.
PA   (ALSO/) ALSOBROOK J P.
PA   (BURG/) BURGESS C E.
PA   (PADI/) PADIGARU M.
PA   (TAYL/) TAYLOR S.
PA   (TCHE/) TCHERNEV V T.
PA   (SPYT/) SPYTEK K A.
PA   (LILL/) LI L.
PA   (SHEN/) SHENOY S.
PA   (KEKU/) KEKUDA R.
PA   (GANG/) GANGOLLI E A.
PA   (STON/) STONE D J.
PA   (SMIT/) SMITHSON G.
PA   (MACD/) MACDOUGALL J R.
 Query Match   5.8%; Score 69.5; DB 7; Length 308;
  Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1288
ID   ABR01671 standard; protein; 316 AA.
DE   Human G protein coupled receptor SEQ ID 202.
PN   WO2003000735-A2.
PD   03-JAN-2003.
PA   (DECO-) DECODE GENETICS EHF.
 Query Match   5.8%; Score 69.5; DB 6; Length 316;
  Best Local Similarity 20.9%; Pred. No. 52;
RESULT 1289
ID   AAY35360 standard; protein; 321 AA.
DE   Chlamydia pneumoniae involved in the virulence process.
PN   WO9927105-A2.
PD   03-JUN-1999.
PA   (GEST) GENSET.
 Query Match   5.8%; Score 69.5; DB 2; Length 321;
  Best Local Similarity 21.4%; Pred. No. 53;
RESULT 1290
ID   ADC33485 standard; protein; 321 AA.
DE   Yeast ARV1.
PN   US6566512-B1.
PD   20-MAY-2003.
PA   (UYCO) UNIV COLUMBIA NEW YORK.
 Query Match   5.8%; Score 69.5; DB 7; Length 321;
  Best Local Similarity 18.8%; Pred. No. 53;
RESULT 1291
ID   ADE37749 standard; protein; 321 AA.
DE   Yeast ARV1 (ARE-2 Required for viability).
PN   US2003186879-A1.
PD   02-OCT-2003.

PA   (UYCO) UNIV COLUMBIA NEW YORK.
  Query Match   5.8%;   Score 69.5;   DB 7;   Length 321;
  Best Local Similarity 18.8%;   Pred. No. 53;
RESULT 1292
ID   AAU53139 standard; protein; 327 AA.
DE   Propionibacterium acnes immunogenic protein #14035.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
  Query Match   5.8%;   Score 69.5;   DB 4;   Length 327;
  Best Local Similarity 25.5%;   Pred. No. 54;
RESULT 1293
ID   ABM49658 standard; protein; 327 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #14334.
PN   WO200033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
  Query Match   5.8%;   Score 69.5;   DB 6;   Length 327;
  Best Local Similarity 25.5%;   Pred. No. 54;
RESULT 1294
ID   ADH10684 standard; protein; 354 AA.
DE   Rat Sprague-Dawley putative GCR polypeptide.
PN   WO2003104484-A1.
PD   18-DEC-2003.
PA   (META-) METABOLEX INC.
  Query Match   5.8%;   Score 69.5;   DB 8;   Length 354;
  Best Local Similarity 22.0%;   Pred. No. 61;
RESULT 1295
ID   AAY05489 standard; protein; 382 AA.
DE   Human EDG-2 protein sequence.
PN   WO919513-A2.
PD   22-APR-1999.
PA   (LXRB-) LXR BIOTECHNOLOGY INC.
  Query Match   5.8%;   Score 69.5;   DB 2;   Length 382;
  Best Local Similarity 20.2%;   Pred. No. 67;
RESULT 1296
ID   AAU00302 standard; protein; 382 AA.
DE   LPA receptor-related amino acid sequence #1.
PN   WO200112838-A2.
PD   22-FEB-2001.
PA   (ATAI-) ATAIRGIN TECHNOLOGIES INC.
  Query Match   5.8%;   Score 69.5;   DB 4;   Length 382;
  Best Local Similarity 20.2%;   Pred. No. 67;
RESULT 1297
ID   ABG76099 standard; protein; 382 AA.
DE   Human lysophosphatidic acid (LPA) receptor EDG-1.
PN   US6485922-B1.
PD   26-NOV-2002.
PA   (ATAI-) ATAIRGIN TECHNOLOGIES INC.
  Query Match   5.8%;   Score 69.5;   DB 6;   Length 382;
  Best Local Similarity 20.2%;   Pred. No. 67;
RESULT 1298
ID   ABB47613 standard; protein; 400 AA.
DE   Listeria monocytogenes protein #317.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
  Query Match   5.8%;   Score 69.5;   DB 5;   Length 400;
  Best Local Similarity 22.9%;   Pred. No. 72;
RESULT 1299
ID   ABU32698 standard; protein; 400 AA.
DE   Protein encoded by Prokaryotic essential gene #18225.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match   5.8%;   Score 69.5;   DB 6;   Length 400;
  Best Local Similarity 22.9%;   Pred. No. 72;
RESULT 1300
ID   ADL12060 standard; protein; 401 AA.
DE   Drosophila dmTrp1 protein.
PN   WO2003002137-A2.
PD   09-JAN-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.

  Query Match   5.8%;   Score 69.5;   DB 7;   Length 401;
  Best Local Similarity 20.9%;   Pred. No. 72;
RESULT 1301
ID   ABB60948 standard; protein; 415 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 9636.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
  Query Match   5.8%;   Score 69.5;   DB 4;   Length 415;
  Best Local Similarity 20.9%;   Pred. No. 75;
RESULT 1302
ID   ADL12059 standard; protein; 415 AA.
DE   Drosophila dmTrp1alt2 protein.
PN   WO2003002137-A2.
PD   09-JAN-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
  Query Match   5.8%;   Score 69.5;   DB 7;   Length 415;
  Best Local Similarity 20.9%;   Pred. No. 75;
RESULT 1303
ID   ABB66992 standard; protein; 428 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 27768.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
  Query Match   5.8%;   Score 69.5;   DB 4;   Length 428;
  Best Local Similarity 20.9%;   Pred. No. 79;
RESULT 1304
ID   ADL12058 standard; protein; 428 AA.
DE   Drosophila dmTrp1alt1 protein.
PN   WO2003002137-A2.
PD   09-JAN-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
  Query Match   5.8%;   Score 69.5;   DB 7;   Length 428;
  Best Local Similarity 20.9%;   Pred. No. 79;
RESULT 1305
ID   AAY41284 standard; protein; 444 AA.
DE   cI-NT-his fusion protein encoded by plasmid pLJM6-09.
PN   WO953033-A1.
PD   21-OCT-1999.
PA   (UYVA-) UNIV VANDERBILT.
  Query Match   5.8%;   Score 69.5;   DB 2;   Length 444;
  Best Local Similarity 23.6%;   Pred. No. 83;
RESULT 1306
ID   AAG30875 standard; protein; 453 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   5.8%;   Score 69.5;   DB 3;   Length 453;
  Best Local Similarity 23.3%;   Pred. No. 85;
RESULT 1307
ID   ADK47327 standard; protein; 453 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 3842.
PN   US6699703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   5.8%;   Score 69.5;   DB 8;   Length 453;
  Best Local Similarity 24.4%;   Pred. No. 85;
RESULT 1308
ID   ADR95087 standard; protein; 461 AA.
DE   Novel S. pneumoniae protein sequence, SEQ ID 3722.
PN   US6800744-B1.
PD   05-OCT-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   5.8%;   Score 69.5;   DB 8;   Length 461;
  Best Local Similarity 24.4%;   Pred. No. 87;
RESULT 1309
ID   AAG30874 standard; protein; 476 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match   5.8%;   Score 69.5;   DB 3;   Length 476;
  Best Local Similarity 23.3%;   Pred. No. 91;
RESULT 1310

ID   ADN22349 standard; protein; 477 AA.
DB   Bacterial polypeptide #5002.
PN   US20030323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 477;
     Best Local Similarity 23.5%; Pred. No. 92;
RESULT 1311
ID   ADS28512 standard; protein; 490 AA.
DB   Bacterial polypeptide #17545.
PN   US20030323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 490;
     Best Local Similarity 21.2%; Pred. No. 95;
RESULT 1312
ID   ABO61637 standard; protein; 494 AA.
DB   Klebsiella pneumoniae polypeptide seqid 8154.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 494;
     Best Local Similarity 22.0%; Pred. No. 96;
RESULT 1313
ID   AAY41278 standard; protein; 500 AA.
DE   Fusion protein containing rabbit prostaglandin E2EP3 receptor.
PN   WO9953033-A1.
PD   21-OCT-1999.
PA   (UYVA-) UNIV VANDERBILT.
     Query Match   5.8%;   Score 69.5;   DB 2;   Length 500;
     Best Local Similarity 23.6%; Pred. No. 98;
RESULT 1314
ID   AAG30873 standard; protein; 503 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36986.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (DIVE-) DIVERSA CORP.
     Query Match   5.8%;   Score 69.5;   DB 3;   Length 503;
     Best Local Similarity 23.3%; Pred. No. 99;
RESULT 1315
ID   AAY92829 standard; protein; 535 AA.
DE   C. pneumoniae CPN100557 processed antigen.
PN   WO200024765-A2.
PD   04-MAY-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
     Query Match   5.8%;   Score 69.5;   DB 3;   Length 535;
     Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1316
ID   ADR13717 standard; protein; 540 AA.
DE   Amidase, SEQ ID 54.
PN   WO2004069848-A2.
PD   19-AUG-2004.
PA   (DIVE-) DIVERSA CORP.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 540;
     Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1317
ID   AAY92828 standard; protein; 547 AA.
DB   C. pneumoniae CPN100557 antigen.
PN   WO200024765-A2.
PD   04-MAY-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
     Query Match   5.8%;   Score 69.5;   DB 3;   Length 547;
     Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1318
ID   ABU26764 standard; protein; 547 AA.
DE   Protein encoded by Prokaryotic essential gene #12291.

PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 547;
     Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1319
ID   ABU31940 standard; protein; 551 AA.
DE   Protein encoded by Prokaryotic essential gene #17467.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 551;
     Best Local Similarity 23.6%; Pred. No. 1.1e+02;
RESULT 1320
ID   AAY01650 standard; protein; 557 AA.
DE   A protein with cation transporting activity.
PN   WO913072-A1.
PD   18-MAR-1999.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
     Query Match   5.8%;   Score 69.5;   DB 2;   Length 557;
     Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1321
ID   AAY83929 standard; protein; 557 AA.
DE   Human carnitine transporter protein OCTN2.
PN   WO20014210-A1.
PD   16-MAR-2000.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
     Query Match   5.8%;   Score 69.5;   DB 3;   Length 557;
     Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1322
ID   ABG03029 standard; protein; 557 AA.
DE   Novel human diagnostic protein #3020.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.8%;   Score 69.5;   DB 4;   Length 557;
     Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1323
ID   ABB82979 standard; protein; 557 AA.
DE   Human SLC22A related protein-GenBank Identifier No. GI# 3242598.
PN   WO200299053-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 557;
     Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1324
ID   ABB82980 standard; protein; 557 AA.
DE   Human SLC22A related protein-GenBank Identifier No. GI# 4507005.
PN   WO200299053-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 557;
     Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1325
ID   ABO07242 standard; protein; 557 AA.
DE   Human p53 modifying protein, SEQ ID 202.
PN   WO200299122-A1.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 557;
     Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1326
ID   ADE09321 standard; protein; 557 AA.
DE   Novel protein-related contig polypeptide sequence #387.
PN   WO200305152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 557;
     Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1327
ID   ADE09261 standard; protein; 557 AA.
DE   Novel protein-related contig polypeptide sequence #327.
PN   WO200305152-A2.

PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 557;
     Best Local Similarity   26.3%;   Pred. No. 1.1e+02;
RESULT 1328
ID   ADP23817 standard; protein; 557 AA.
DE   PRO polypeptide SEQ ID NO:995.
PN   WO200404170-A2.
PD   21-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 557;
     Best Local Similarity   26.3%;   Pred. No. 1.1e+02;
RESULT 1329
ID   ADA34637 standard; protein; 559 AA.
DE   Acinetobacter baumannii protein #1798.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 559;
     Best Local Similarity   20.2%;   Pred. No. 1.1e+02;
RESULT 1330
ID   ABO62908 standard; protein; 564 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9425.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 559;
     Best Local Similarity   23.6%;   Pred. No. 1.2e+02;
RESULT 1331
ID   ABB89665 standard; protein; 568 AA.
DE   Human polypeptide SEQ ID NO 2041.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   5.8%;   Score 69.5;   DB 5;   Length 568;
     Best Local Similarity   22.4%;   Pred. No. 1.2e+02;
RESULT 1332
ID   ADB65515 standard; protein; 573 AA.
DE   Human protein encoded by clone TESTI20271790.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 573;
     Best Local Similarity   22.7%;   Pred. No. 1.2e+02;
RESULT 1333
ID   ABB47410 standard; protein; 579 AA.
DE   Listeria monocytogenes protein #114.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
     Query Match   5.8%;   Score 69.5;   DB 5;   Length 579;
     Best Local Similarity   21.1%;   Pred. No. 1.2e+02;
RESULT 1334
ID   ABU32703 standard; protein; 579 AA.
DE   Protein encoded by Prokaryotic essential gene #18230.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 579;
     Best Local Similarity   21.1%;   Pred. No. 1.2e+02;
RESULT 1335
ID   ABP65234 standard; protein; 599 AA.
DE   Hypoxia-regulated protein #108.
PN   WO200246465-A2.
PD   13-JUN-2002.
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
     Query Match   5.8%;   Score 69.5;   DB 5;   Length 599;
     Best Local Similarity   19.6%;   Pred. No. 1.3e+02;
RESULT 1336
ID   AAE38584 standard; protein; 599 AA.
DE   Human GAT1 GABA transporter protein.
PN   WO2003061573-A2.

PD   31-JUL-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 599;
     Best Local Similarity   19.6%;   Pred. No. 1.3e+02;
RESULT 1337
ID   ADD46025 standard; protein; 599 AA.
DE   Human Protein P30531, SEQ ID NO 11697.
PN   WO200301675-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 599;
     Best Local Similarity   19.6%;   Pred. No. 1.3e+02;
RESULT 1338
ID   AAY41285 standard; protein; 656 AA.
DE   cI-77A-TL fusion protein encoded by plasmid pLJM5-42T.
PN   WO9953033-A1.
PD   21-OCT-1999.
PA   (UYVA-) UNIV VANDERBILT.
     Query Match   5.8%;   Score 69.5;   DB 2;   Length 656;
     Best Local Similarity   23.6%;   Pred. No. 1.4e+02;
RESULT 1339
ID   ABP40194 standard; protein; 660 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;   Score 69.5;   DB 5;   Length 660;
     Best Local Similarity   27.2%;   Pred. No. 1.4e+02;
RESULT 1340
ID   ADS07250 standard; protein; 660 AA.
DE   Staphylococcus epidermis polypeptide seqid 6545.
PN   US2004147734-A1.
PD   29-JUL-2004.
PA   (DOUC/) DOUCETTE-STAMM L.
PA   (BUSH/) BUSH D.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 660;
     Best Local Similarity   27.2%;   Pred. No. 1.4e+02;
RESULT 1341
ID   AAY17390 standard; protein; 663 AA.
DE   Human vesicle membrane protein-like protein 3.
PN   WO9921994-A2.
PD   06-MAY-1999.
PA   (INCY-) INCYTE PHARM INC.
     Query Match   5.8%;   Score 69.5;   DB 2;   Length 663;
     Best Local Similarity   22.0%;   Pred. No. 1.4e+02;
RESULT 1342
ID   ADM83092 standard; protein; 663 AA.
DE   Human vesicle membrane protein (VMP)2.
PN   US2003175787-A1.
PD   18-SEP-2003.
PA   (INCY-) INCYTE CORP.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 663;
     Best Local Similarity   22.0%;   Pred. No. 1.4e+02;
RESULT 1343
ID   ADJ64317 standard; protein; 663 AA.
DE   Cartilage differentiation inhibiting protein, SEQ ID 12.
PN   WO200401326-A1.
PD   12-FEB-2004.
PA   (ASAH) ASAHI KASEI KK.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 663;
     Best Local Similarity   22.0%;   Pred. No. 1.4e+02;
RESULT 1344
ID   ADQ96536 standard; protein; 663 AA.
DE   T cell activation associated protein #357.
PN   WO200405805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 663;
     Best Local Similarity   22.0%;   Pred. No. 1.4e+02;
RESULT 1345
ID   ADO09827 standard; protein; 681 AA.
DE   Hamster SGLT homologue protein SEQ ID NO:50.

PN   WO2004039405-A1.
PD   13-MAY-2004.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 681;
     Best Local Similarity   24.5%;   Pred. No. 1.5e+02;
RESULT 1346
ID   ABU41908 standard; protein; 695 AA.
DE   Protein encoded by Prokaryotic essential gene #27435.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 695;
     Best Local Similarity   24.3%;   Pred. No. 1.5e+02;
RESULT 1347
ID   ADJ48367 standard; protein; 764 AA.
DE   Maize oil-associated gene protein #26.
PN   US2004025202-A1.
PD   05-FEB-2004.
PA   (LAUR/) LAURIE C C.
PA   (RAVA/) RAVANELLO M.
PA   (SAVA/) SAVAGE T.
PA   (LEDE/) LEDEAUX J R.
PA   (ROGE/) ROGERS J A.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 764;
     Best Local Similarity   21.0%;   Pred. No. 1.8e+02;
RESULT 1348
ID   ABU43821 standard; protein; 801 AA.
DE   Protein encoded by Prokaryotic essential gene #29348.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 801;
     Best Local Similarity   19.9%;   Pred. No. 1.9e+02;
RESULT 1349
ID   AAY70245 standard; protein; 805 AA.
DE   Human Polycystin-L protein.
PN   WO200012046-A2.
PD   09-MAR-2000.
PA   (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
     Query Match   5.8%;   Score 69.5;   DB 3;   Length 805;
     Best Local Similarity   20.4%;   Pred. No. 1.9e+02;
RESULT 1350
ID   ABB98140 standard; protein; 863 AA.
DE   Human PMMM Incyte ID 7484157CD1.
PN   WO200246383-A2.
PD   13-JUN-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   5.8%;   Score 69.5;   DB 5;   Length 863;
     Best Local Similarity   19.3%;   Pred. No. 2.1e+02;
RESULT 1351
ID   AAY96168 standard; protein; 877 AA.
DE   Bacterial polypeptide #22547.
PN   US2003223675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 877;
     Best Local Similarity   22.7%;   Pred. No. 2.1e+02;
RESULT 1352
ID   ADS44117 standard; protein; 877 AA.

RESULT 1353
ID   AAG70761 standard; protein; 881 AA.
DE   S cerevisiae apoptosis associated protein YJL197W.
PN   WO200102550-A2.
PD   11-JAN-2001.
PA   (JANC) JANSSEN PHARM NV.
     Query Match   5.8%;   Score 69.5;   DB 4;   Length 881;
     Best Local Similarity   24.4%;   Pred. No. 2.1e+02;
RESULT 1354
ID   ABU16635 standard; protein; 1010 AA.
DE   Protein encoded by Prokaryotic essential gene #2162.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 1010;
     Best Local Similarity   24.7%;   Pred. No. 2.6e+02;
RESULT 1355
ID   ADA34462 standard; protein; 1028 AA.
DE   Acinetobacter baumannii protein #1623.
PN   US6652958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;   Score 69.5;   DB 6;   Length 1028;
     Best Local Similarity   24.7%;   Pred. No. 2.7e+02;
RESULT 1356
ID   AAW25671 standard; protein; 1684 AA.
DE   hABC3 protein.
PN   WO9702346-A2.
PD   23-JAN-1997.
PA   (GENZ) GENZYME CORP.
     Query Match   5.8%;   Score 69.5;   DB 2;   Length 1684;
     Best Local Similarity   20.3%;   Pred. No. 5.3e+02;
RESULT 1357
ID   AAW46761 standard; protein; 1684 AA.
DE   Amino acid sequence of human ATP binding cassette transporter.
PN   WO9748797-A1.
PD   24-DEC-1997.
PA   (GENZ) GENZYME CORP.
     Query Match   5.8%;   Score 69.5;   DB 2;   Length 1684;
     Best Local Similarity   20.3%;   Pred. No. 5.3e+02;
RESULT 1358
ID   AAW46771 standard; protein; 1704 AA.
DE   Amino acid sequence of human ATP binding cassette transporter.
PN   WO9748797-A1.
PD   24-DEC-1997.
PA   (GENZ) GENZYME CORP.
     Query Match   5.8%;   Score 69.5;   DB 2;   Length 1704;
     Best Local Similarity   20.3%;   Pred. No. 5.4e+02;
RESULT 1359
ID   ABP52094 standard; protein; 1704 AA.
DE   Homo sapiens ABC transporter ABCA3 protein SEQ ID NO:46.
PN   EP1217066-A1.
PD   26-JUN-2002.
PA   (UYGE-) UNIV GENT.
     Query Match   5.8%;   Score 69.5;   DB 5;   Length 1704;
     Best Local Similarity   20.3%;   Pred. No. 5.4e+02;
RESULT 1360
ID   ADJ70414 standard; protein; 1704 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID2220.
PN   WO2003087768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match   5.8%;   Score 69.5;   DB 7;   Length 1704;
     Best Local Similarity   20.3%;   Pred. No. 5.4e+02;
RESULT 1361
ID   ADL61289 standard; protein; 1704 AA.
DE   Human ATP-binding cassette subfamily A (ABC1) member 3 protein.
PN   WO2004020583-A2.
PD   11-MAR-2004.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
     Query Match   5.8%;   Score 69.5;   DB 8;   Length 1704;
     Best Local Similarity   20.3%;   Pred. No. 5.4e+02;

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RESULT 1362
ID   ADB09274 standard; protein; 154 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:3214.
PN   WO2003048304-A2.
PD   12-JUN-2003.
PA   (AMHP ) WYETH HOLDINGS CORP.
     Query Match             5.8%;  Score 69;  DB 6;  Length 154;
     Best Local Similarity  27.3%;  Pred. No. 22;
RESULT 1363
ID   ADK16543 standard; protein; 178 AA.
DE   Nanoarchaeum equitans cancer-associated (CA) protein #247.
PN   WO2003093434-A2.
PD   13-NOV-2003.
PA   (DIVE-) DIVERSA CORP.
     Query Match             5.8%;  Score 69;  DB 8;  Length 178;
     Best Local Similarity  23.3%;  Pred. No. 27;
RESULT 1364
ID   AAU65589 standard; protein; 191 AA.
DE   Propionibacterium acnes immunogenic protein #26485.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
     Query Match             5.8%;  Score 69;  DB 4;  Length 191;
     Best Local Similarity  26.6%;  Pred. No. 29;
RESULT 1365
ID   ABM62108 standard; protein; 191 AA.
DE   Propionibacterium acnes permease/transporter-related polypeptide #26784.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
     Query Match             5.8%;  Score 69;  DB 6;  Length 191;
     Best Local Similarity  26.6%;  Pred. No. 29;
RESULT 1366
ID   AAW38633 standard; protein; 193 AA.
DE   S. pneumoniae LPLC protein.
PN   WO9743303-A1.
PD   20-NOV-1997.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
     Query Match             5.8%;  Score 69;  DB 2;  Length 193;
     Best Local Similarity  28.3%;  Pred. No. 30;
RESULT 1367
ID   AAB21047 standard; protein; 214 AA.
DE   Human nucleic acid-binding protein, NuABP-51.
PN   WO200044900-A2.
PD   03-AUG-2000.
PA   (INCY-) INCYTE PHARM INC.
     Query Match             5.8%;  Score 69;  DB 3;  Length 214;
     Best Local Similarity  24.7%;  Pred. No. 34;
RESULT 1368
ID   ABP58238 standard; protein; 214 AA.
DE   Human ovary-specific O1-236 (NPM2) protein.
PN   WO200288314-A2.
PD   07-NOV-2002.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (AMHP ) WYETH.
     Query Match             5.8%;  Score 69;  DB 6;  Length 214;
     Best Local Similarity  24.7%;  Pred. No. 34;
RESULT 1369
ID   ADJ63172 standard; protein; 214 AA.
DE   Human nucleoplasmin (Npm2) protein.
PN   WO2003091400-A2.
PD   06-NOV-2003.
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (AMHP ) WYETH.
     Query Match             5.8%;  Score 69;  DB 7;  Length 214;
     Best Local Similarity  24.7%;  Pred. No. 34;
RESULT 1370
ID   ADM03849 standard; protein; 214 AA.
DE   Human protein of the invention SEQ ID NO:2534.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match             5.8%;  Score 69;  DB 7;  Length 214;
     Best Local Similarity  24.7%;  Pred. No. 34;
RESULT 1371
ID   ADN46858 standard; protein; 239 AA.
DE   Thermococcus kodakaraensis KOD1 protein sequence SeqID736.
PN   WO2004022736-A1.
PD   18-MAR-2004.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
     Query Match             5.8%;  Score 69;  DB 8;  Length 239;
     Best Local Similarity  23.5%;  Pred. No. 40;
RESULT 1372
ID   ABM69545 standard; protein; 337 AA.
DE   Photorhabdus luminescens protein sequence #2642.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             5.8%;  Score 69;  DB 6;  Length 337;
     Best Local Similarity  19.8%;  Pred. No. 65;
RESULT 1373
ID   ABM72781 standard; protein; 350 AA.
DE   Staphylococcus aureus protein #2021.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match             5.8%;  Score 69;  DB 6;  Length 350;
     Best Local Similarity  20.5%;  Pred. No. 68;
RESULT 1374
ID   AAG04120 standard; protein; 356 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 27.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match             5.8%;  Score 69;  DB 3;  Length 356;
     Best Local Similarity  21.0%;  Pred. No. 70;
RESULT 1375
ID   AAR91218 standard; protein; 370 AA.
DE   Human pituitary G-protein coupled receptor protein.
PN   WO9605302-A1.
PD   22-FEB-1996.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             5.8%;  Score 69;  DB 2;  Length 370;
     Best Local Similarity  21.8%;  Pred. No. 74;
RESULT 1376
ID   AAW31379 standard; protein; 370 AA.
DE   Human G protein-coupled receptor protein from phGR3.
PN   WO9724436-A2.
PD   10-JUL-1997.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             5.8%;  Score 69;  DB 2;  Length 370;
     Best Local Similarity  21.8%;  Pred. No. 74;
RESULT 1377
ID   AAW95181 standard; peptide; 370 AA.
DE   Human G-protein coupled receptor polypeptide.
PN   WO9849295-A1.
PD   05-NOV-1998.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             5.8%;  Score 69;  DB 2;  Length 370;
     Best Local Similarity  21.8%;  Pred. No. 74;
RESULT 1378
ID   AAW97221 standard; peptide; 370 AA.
DE   Human pituitary-derived G protein-coupled receptor protein.
PN   WO985962-A1.
PD   30-DEC-1998.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match             5.8%;  Score 69;  DB 2;  Length 370;
     Best Local Similarity  21.8%;  Pred. No. 74;
RESULT 1379
ID   AAG04119 standard; protein; 370 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 26.
PN   EP103405-A2.
PD   06-SEP-2000.
     Query Match             5.8%;  Score 69;  DB 3;  Length 370;
     Best Local Similarity  21.0%;  Pred. No. 74;
```

RESULT 1380
ID AAG62539 standard; protein; 370 AA.
DB Human CRH releasing protein related protein SEQ ID NO: 46.
PN WO200135984-A1.
PD 25-MAY-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
    Query Match   5.8%;   Score 69; DB 4; Length 370;
    Best Local Similarity 21.8%;   Pred. No. 74;

RESULT 1381
ID ABP81880 standard; protein; 370 AA.
DB Human G protein-coupled receptor 10 protein SEQ ID NO:245.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
    Query Match   5.8%;   Score 69; DB 6; Length 370;
    Best Local Similarity 21.8%;   Pred. No. 74;

RESULT 1382
ID ADO29365 standard; protein; 370 AA.
DB Human GPCR GPR10, SEQ ID NO:466.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
    Query Match   5.8%;   Score 69; DB 8; Length 370;
    Best Local Similarity 21.8%;   Pred. No. 74;

RESULT 1383
ID AAW27510 standard; protein; 380 AA.
DB Consensus human hypothalamic receptor.
PN WO9708317-A2.
PD 06-MAR-1997.
PA (CHIR) CHIRON CORP.
    Query Match   5.8%;   Score 69; DB 2; Length 380;
    Best Local Similarity 21.8%;   Pred. No. 76;

RESULT 1384
ID AAB16020 standard; protein; 388 AA.
DB E. coli proliferation associated protein sequence SEQ ID NO:378.
PN WO200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   5.8%;   Score 69; DB 3; Length 388;
    Best Local Similarity 27.2%;   Pred. No. 79;

RESULT 1385
ID AAG98322 standard; protein; 388 AA.
DB Escherichia coli protein sequence SEQ ID NO:370.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   5.8%;   Score 69; DB 4; Length 388;
    Best Local Similarity 27.2%;   Pred. No. 79;

RESULT 1386
ID ABU14818 standard; protein; 388 AA.
DB Protein encoded by Prokaryotic essential gene #345.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   5.8%;   Score 69; DB 6; Length 388;
    Best Local Similarity 27.2%;   Pred. No. 79;

RESULT 1387
ID ADS45229 standard; protein; 437 AA.
DB Bacterial polypeptide #23659.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
    Query Match   5.8%;   Score 69; DB 8; Length 437;
    Best Local Similarity 22.4%;   Pred. No. 93;

RESULT 1388
ID ABO61901 standard; protein; 472 AA.
DB Klebsiella pneumoniae polypeptide seqid 8418.
PN US6610836-B1.
PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   5.8%;   Score 69; DB 7; Length 472;
    Best Local Similarity 21.3%;   Pred. No. 1e+02;

RESULT 1389
ID AAG42138 standard; protein; 508 AA.
DB Arabidopsis thaliana protein fragment SEQ ID NO: 52514.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   5.8%;   Score 69; DB 3; Length 508;
    Best Local Similarity 20.2%;   Pred. No. 1.1e+02;

RESULT 1390
ID AAG04118 standard; protein; 509 AA.
DB Arabidopsis thaliana protein fragment SEQ ID NO: 25.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   5.8%;   Score 69; DB 3; Length 509;
    Best Local Similarity 21.0%;   Pred. No. 1.1e+02;

RESULT 1391
ID AAG42137 standard; protein; 520 AA.
DB Arabidopsis thaliana protein fragment SEQ ID NO: 52513.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   5.8%;   Score 69; DB 3; Length 520;
    Best Local Similarity 20.2%;   Pred. No. 1.2e+02;

RESULT 1392
ID ABB59760 standard; protein; 593 AA.
DB Drosophila melanogaster polypeptide SEQ ID NO 6072.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
    Query Match   5.8%;   Score 69; DB 4; Length 593;
    Best Local Similarity 22.7%;   Pred. No. 1.4e+02;

RESULT 1393
ID AAG31959 standard; protein; 609 AA.
DB Arabidopsis thaliana protein fragment SEQ ID NO: 38469.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   5.8%;   Score 69; DB 3; Length 609;
    Best Local Similarity 21.0%;   Pred. No. 1.5e+02;

RESULT 1394
ID AAG31958 standard; protein; 624 AA.
DB Arabidopsis thaliana protein fragment SEQ ID NO: 38468.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   5.8%;   Score 69; DB 3; Length 624;
    Best Local Similarity 21.0%;   Pred. No. 1.5e+02;

RESULT 1395
ID AAE05101 standard; protein; 641 AA.
DB Drosophila melanogaster dmKSNF.
PN WO200149848-A2.
PD 12-JUL-2001.
PA (GENO-) GENOPTERA LLC.
    Query Match   5.8%;   Score 69; DB 4; Length 641;
    Best Local Similarity 22.7%;   Pred. No. 1.6e+02;

RESULT 1396
ID AAG31957 standard; protein; 659 AA.
DB Arabidopsis thaliana protein fragment SEQ ID NO: 38467.
PN EP103405-A2.
PD 06-SEP-2000.
    Query Match   5.8%;   Score 69; DB 3; Length 659;
    Best Local Similarity 21.0%;   Pred. No. 1.6e+02;

RESULT 1397
ID ABB11769 standard; peptide; 666 AA.
DB Human dJ37C10.3 ATPase homologue, SEQ ID NO:2139.
PN WO20015718B-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   5.8%;   Score 69; DB 3; Length 666;
    Best Local Similarity 23.4%;   Pred. No. 1.7e+02;

RESULT 1398
ID AAM79751 standard; protein; 666 AA.
DB Human protein SEQ ID NO 3397.
PN WO20015719O-A2.

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PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
    Query Match   5.8%;   Score 69;   DB 4; Length 666;
    Best Local Similarity   23.4%;   Pred. No. 1.7e+02;
RESULT 1399
ID ADF05168 standard; protein; 681 AA.
DE Bacterial polypeptide #1281.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   5.8%;   Score 69;   DB 7; Length 681;
    Best Local Similarity   21.5%;   Pred. No. 1.7e+02;
RESULT 1400
ID ABO52988 standard; protein; 791 AA.
DE Human putative spliceosome associated protein (SAP) #52.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
    Query Match   5.8%;   Score 69;   DB 6; Length 791;
    Best Local Similarity   24.8%;   Pred. No. 2.1e+02;
RESULT 1401
ID AAB42779 standard; protein; 792 AA.
DE Human ORFX ORF2543 polypeptide sequence SEQ ID NO:5086.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
    Query Match   5.8%;   Score 69;   DB 3; Length 792;
    Best Local Similarity   24.8%;   Pred. No. 2.1e+02;
RESULT 1402
ID ABP62960 standard; protein; 875 AA.
DE Human polypeptide SEQ ID NO 397.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
    Query Match   5.8%;   Score 69;   DB 5; Length 875;
    Best Local Similarity   24.8%;   Pred. No. 2.4e+02;
RESULT 1403
ID ABM85143 standard; protein; 891 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5392.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
    Query Match   5.8%;   Score 69;   DB 8; Length 891;
    Best Local Similarity   19.5%;   Pred. No. 2.5e+02;
RESULT 1404
ID ABB90877 standard; protein; 1933 AA.
DE Herbicidally active polypeptide SEQ ID NO 88.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
    Query Match   5.8%;   Score 69;   DB 5; Length 1933;
    Best Local Similarity   24.8%;   Pred. No. 7.3e+02;
RESULT 1405
ID ADI95303 standard; protein; 2280 AA.
DE OSPF-related Hepatitis C virus (HCV) polyprotein.
PN WO2004002415-A2.
PD 08-JAN-2004.
PA (DAND) DANA FARBER CANCER INST INC.
    Query Match   5.8%;   Score 69;   DB 8; Length 2280;
    Best Local Similarity   26.9%;   Pred. No. 9.2e+02;
RESULT 1406
ID ADM68764 standard; protein; 5127 AA.
DE Peregrinus maidis ryanodine receptor protein SEQ ID NO:8.
PN WO2004027042-A2.
PD 01-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO B I.
    Query Match   5.8%;   Score 69;   DB 8; Length 5127;
    Best Local Similarity   20.1%;   Pred. No. 2.8e+03;
RESULT 1407
ID ADH85829 standard; protein; 178 AA.
DE Enterococcus faecalis polypeptide #309.
PN US6617156-B1.

PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
    Query Match   5.7%;   Score 68.5; DB 7; Length 178;
    Best Local Similarity   30.7%;   Pred. No. 31;
RESULT 1408
ID ABJ01003 standard; protein; 209 AA.
DE Human breast specific protein SEQ ID NO: 86.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
    Query Match   5.7%;   Score 68.5; DB 5; Length 209;
    Best Local Similarity   21.8%;   Pred. No. 38;
RESULT 1409
ID AAG53772 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68492.
PN EP1033405-A2.
PD 06-SEP-2000.
    Query Match   5.7%;   Score 68.5; DB 3; Length 218;
    Best Local Similarity   40.7%;   Pred. No. 41;
RESULT 1410
ID AAG25640 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29784.
PN EP1033405-A2.
PD 06-SEP-2000.
    Query Match   5.7%;   Score 68.5; DB 3; Length 218;
    Best Local Similarity   40.7%;   Pred. No. 41;
RESULT 1411
ID AAG53747 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68458.
PN EP1033405-A2.
PD 06-SEP-2000.
    Query Match   5.7%;   Score 68.5; DB 3; Length 218;
    Best Local Similarity   40.7%;   Pred. No. 41;
RESULT 1412
ID ADF07413 standard; protein; 225 AA.
DE Bacterial polypeptide #3526.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   5.7%;   Score 68.5; DB 7; Length 225;
    Best Local Similarity   18.2%;   Pred. No. 42;
RESULT 1413
ID ADO57686 standard; protein; 227 AA.
DE Actinobacillus actinomycetemcomitans immunogenic polypeptide #68.
PN WO2004054999-A2.
PD 03-JUN-2004.
PA (UYFL) UNIV FLORIDA.
    Query Match   5.7%;   Score 68.5; DB 8; Length 227;
    Best Local Similarity   24.3%;   Pred. No. 43;
RESULT 1414
ID ADA14398 standard; protein; 278 AA.
DE Mouse spermatogenesis related protein sequence SEQ ID NO:140.
PN WO200306896-A1.
PD 21-AUG-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
    Query Match   5.7%;   Score 68.5; DB 6; Length 278;
    Best Local Similarity   29.2%;   Pred. No. 57;
RESULT 1415
ID ABU29281 standard; protein; 322 AA.
DE Protein encoded by Prokaryotic essential gene #14808.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
    Query Match   5.7%;   Score 68.5; DB 6; Length 322;
    Best Local Similarity   30.7%;   Pred. No. 70;
RESULT 1416
ID ABB99751 standard; protein; 327 AA.
DE Amino acid sequence of bacteriophage phiCpn1 antigenic protein.
PN WO200295413-A2.
PD 28-NOV-2002.
PA (UYBR-) UNIV BRITISH COLUMBIA.
    Query Match   5.7%;   Score 68.5; DB 6; Length 327;

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    Best Local Similarity    27.0%;    Pred. No. 71;
RESULT 1417
ID   AAW25926 standard; protein; 354 AA.
DE   Xenopus melatonin receptor MEL-1Aa.
PN   WO9704094-A1.
PD   06-FEB-1997.
PA   (ADIR ) ADIR & CIE.
     Query Match    5.7%;    Score 68.5;    DB 2;    Length 354;
     Best Local Similarity    18.8%;    Pred. No. 79;
RESULT 1418
ID   AAY87506 standard; protein; 369 AA.
DE   Human G coupled-protein receptor, GPR10.
PN   WO200017641-A1.
PD   30-MAR-2000.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match    5.7%;    Score 68.5;    DB 3;    Length 369;
     Best Local Similarity    23.3%;    Pred. No. 84;
RESULT 1419
ID   AAE13430 standard; protein; 377 AA.
DE   Brassica napus microsomal omega-3 desaturase, bnFAD3 protein.
PN   WO200179499-A1.
PD   25-OCT-2001.
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
     Query Match    5.7%;    Score 68.5;    DB 4;    Length 377;
     Best Local Similarity    29.3%;    Pred. No. 87;
RESULT 1420
ID   AAB28521 standard; protein; 382 AA.
DE   Mouse EDG1 polypeptide.
PN   WO200059529-A1.
PD   12-OCT-2000.
PA   (SMK ) SMITHKLINE BEECHAM CORP.
     Query Match    5.7%;    Score 68.5;    DB 3;    Length 382;
     Best Local Similarity    19.8%;    Pred. No. 88;
RESULT 1421
ID   ABM85456 standard; protein; 382 AA.
DE   Mouse protein sequence mCP20760.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
     Query Match    5.7%;    Score 68.5;    DB 7;    Length 382;
     Best Local Similarity    19.8%;    Pred. No. 88;
RESULT 1422
ID   ADO29286 standard; protein; 382 AA.
DE   Mouse GPCR EDG1, SEQ ID NO:387.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match    5.7%;    Score 68.5;    DB 8;    Length 382;
     Best Local Similarity    19.8%;    Pred. No. 88;
RESULT 1423
ID   ADR67019 standard; protein; 382 AA.
DE   Mouse cancer associated protein sequence SEQ ID NO:65.
PN   WO2004074321-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match    5.7%;    Score 68.5;    DB 8;    Length 382;
     Best Local Similarity    19.8%;    Pred. No. 88;
RESULT 1424
ID   AAW01664 standard; protein; 383 AA.
DE   p(rat-edg), G-protein coupled receptor.
PN   US5585476-A.
PD   17-DEC-1996.
PA   (MACL/) MACLENNAN A J.
     Query Match    5.7%;    Score 68.5;    DB 2;    Length 383;
     Best Local Similarity    19.8%;    Pred. No. 89;
RESULT 1425
ID   AAW87791 standard; protein; 383 AA.
DE   Rat-edg, G-protein coupled receptor superfamily member.
PN   US5855443-A.
PD   05-JAN-1999.
PA   (MACL/) MACLENNAN A J.
     Query Match    5.7%;    Score 68.5;    DB 2;    Length 383;
     Best Local Similarity    19.8%;    Pred. No. 89;

RESULT 1426
ID   ABU61817 standard; protein; 383 AA.
DE   Rat-edg.
PN   US6518414-B1.
PD   11-FEB-2003.
PA   (MACL/) MACLENNAN A J.
     Query Match    5.7%;    Score 68.5;    DB 7;    Length 383;
     Best Local Similarity    19.8%;    Pred. No. 89;
RESULT 1427
ID   ABG07020 standard; protein; 404 AA.
DE   Novel human diagnostic protein #7011.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSB-) HYSEQ INC.
     Query Match    5.7%;    Score 68.5;    DB 4;    Length 404;
     Best Local Similarity    22.4%;    Pred. No. 95;
RESULT 1428
ID   AAB68619 standard; protein; 411 AA.
DE   Human PAC 1 receptor isoform 30.
PN   WO20010478-A1.
PD   01-FEB-2001.
PA   (MEDI-) MEDICAL RES COUNCIL.
     Query Match    5.7%;    Score 68.5;    DB 4;    Length 411;
     Best Local Similarity    29.9%;    Pred. No. 98;
RESULT 1429
ID   ADH87117 standard; protein; 417 AA.
DE   Enterococcus faecalis polypeptide #1597.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match    5.7%;    Score 68.5;    DB 7;    Length 417;
     Best Local Similarity    23.2%;    Pred. No. 1e+02;
RESULT 1430
ID   AAR88409 standard; protein; 420 AA.
DE   High-affinity melatonin receptor.
PN   WO935320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
     Query Match    5.7%;    Score 68.5;    DB 2;    Length 420;
     Best Local Similarity    18.8%;    Pred. No. 1e+02;
RESULT 1431
ID   AAW88344 standard; protein; 430 AA.
DE   Salmonella enterica O antigen pathway flippase protein.
PN   WO9850531-A1.
PD   12-NOV-1998.
PA   (UNSY ) UNIV SYDNEY.
     Query Match    5.7%;    Score 68.5;    DB 2;    Length 430;
     Best Local Similarity    23.6%;    Pred. No. 1e+02;
RESULT 1432
ID   AAU02941 standard; protein; 431 AA.
DE   Angiotensin converting enzyme (ACEV) splice variant protein #41.
PN   WO200136632-A2.
PD   25-MAY-2001.
PA   (COMP-) COMPUGEN LTD.
     Query Match    5.7%;    Score 68.5;    DB 4;    Length 431;
     Best Local Similarity    29.9%;    Pred. No. 1e+02;
RESULT 1433
ID   ADA33815 standard; protein; 437 AA.
DE   Acinetobacter baumannii protein #976.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match    5.7%;    Score 68.5;    DB 6;    Length 437;
     Best Local Similarity    20.5%;    Pred. No. 1.1e+02;
RESULT 1434
ID   ADS12084 standard; protein; 443 AA.
DE   Human therapeutic contig protein - SEQ ID 2321.
PN   WO2004080148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
     Query Match    5.7%;    Score 68.5;    DB 8;    Length 443;
     Best Local Similarity    19.6%;    Pred. No. 1.1e+02;
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RESULT 1435
ID   AAB71866 standard; protein; 444 AA.
DE   Human CRP1 seven transmembrane domain.
PN   WO200109328-A1.
PD   08-FEB-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   5.7%;   Score 68.5;   DB 4;   Length 444;
     Best Local Similarity   23.7%;   Pred. No. 1.1e+02;

RESULT 1436
ID   AAB26685 standard; protein; 444 AA.
DE   Human CRP-RA2 splice variant protein.
PN   US2002055617-A1.
PD   09-MAY-2002.
PA   (PERR/) PERRIN M H.
PA   (CHEN/) CHEN R.
PA   (LEWI/) LEWIS K A.
PA   (VALE/) VALE W W.
PA   (DONA/) DONALDSON C J.
PA   (SAWC/) SAWCHENKO P.
     Query Match   5.7%;   Score 68.5;   DB 5;   Length 444;
     Best Local Similarity   23.7%;   Pred. No. 1.1e+02;

RESULT 1437
ID   ABR43052 standard; protein; 444 AA.
DE   Human CRH-R1 beta protein SEQ ID NO:2.
PN   WO200302499O-A2.
PD   27-MAR-2003.
PA   (UYTE-) UNIV TENNESSEE RES CORP.
     Query Match   5.7%;   Score 68.5;   DB 6;   Length 444;
     Best Local Similarity   23.7%;   Pred. No. 1.1e+02;

RESULT 1438
ID   ABU08081 standard; protein; 444 AA.
DE   Human corticotropin-releasing factor receptor 2 (CRF-R2).
PN   US6495343-B1.
PD   17-DEC-2002.
PA   (SALK) SALK INST BIOLOGICAL STUDIES.
     Query Match   5.7%;   Score 68.5;   DB 6;   Length 444;
     Best Local Similarity   23.7%;   Pred. No. 1.1e+02;

RESULT 1439
ID   ABG76402 standard; protein; 444 AA.
DE   Human hCRF-RA1, splice variant.
PN   US6482608-B1.
PD   19-NOV-2002.
PA   (SALK) SALK INST BIOLOGICAL STUDIES.
     Query Match   5.7%;   Score 68.5;   DB 6;   Length 444;
     Best Local Similarity   23.7%;   Pred. No. 1.1e+02;

RESULT 1440
ID   ADB62734 standard; protein; 444 AA.
DE   Human Protein P34998, SEQ ID NO 8667.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
     Query Match   5.7%;   Score 68.5;   DB 7;   Length 444;
     Best Local Similarity   23.7%;   Pred. No. 1.1e+02;

RESULT 1441
ID   ADJ65810 standard; protein; 444 AA.
DE   Human corticotropin-releasing factor receptor CRF-RA2.
PN   US2004039173-A1.
PD   26-FEB-2004.
PA   (SALK) SALK INST BIOLOGICAL STUDIES.
     Query Match   5.7%;   Score 68.5;   DB 8;   Length 444;
     Best Local Similarity   23.7%;   Pred. No. 1.1e+02;

RESULT 1442
ID   ADC86255 standard; protein; 447 AA.
DE   Human GPCR protein SEQ ID NO:708.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
     Query Match   5.7%;   Score 68.5;   DB 7;   Length 447;
     Best Local Similarity   23.7%;   Pred. No. 1.1e+02;

RESULT 1443
ID   AAR58668 standard; protein; 448 AA.
DE   Human PACAP receptor type 1A mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.7%;   Score 68.5;   DB 2;   Length 448;
     Best Local Similarity   29.9%;   Pred. No. 1.1e+02;

RESULT 1444
ID   ABB56380 standard; protein; 468 AA.
DE   Non-endogenous human GPCR protein, SEQ ID NO: 553.
PN   WO200177172-A2.
PD   18-OCT-2001.
PA   (AREN-) ARENA PHARM INC.
     Query Match   5.7%;   Score 68.5;   DB 4;   Length 468;
     Best Local Similarity   29.9%;   Pred. No. 1.2e+02;

RESULT 1445
ID   AAB71874 standard; protein; 468 AA.
DE   Human PACR seven transmembrane domain.
PN   WO200109328-A1.
PD   08-FEB-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   5.7%;   Score 68.5;   DB 4;   Length 468;
     Best Local Similarity   29.9%;   Pred. No. 1.2e+02;

RESULT 1446
ID   ADC86185 standard; protein; 468 AA.
DE   Human GPCR protein SEQ ID NO:638.
PN   EP1270724-A2.
PD   02-JAN-2003.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
     Query Match   5.7%;   Score 68.5;   DB 7;   Length 468;
     Best Local Similarity   29.9%;   Pred. No. 1.2e+02;

RESULT 1447
ID   ADO29153 standard; protein; 468 AA.
DE   Human GPCR ADCYAP1R1, SEQ ID NO:254.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match   5.7%;   Score 68.5;   DB 7;   Length 468;
     Best Local Similarity   29.9%;   Pred. No. 1.2e+02;

RESULT 1448
ID   AAR58670 standard; protein; 475 AA.
DE   Human PACAP receptor type 1-B2 mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.7%;   Score 68.5;   DB 2;   Length 475;
     Best Local Similarity   29.9%;   Pred. No. 1.2e+02;

RESULT 1449
ID   AAR58671 standard; protein; 476 AA.
DE   Human PACAP receptor type 1C mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.7%;   Score 68.5;   DB 2;   Length 476;
     Best Local Similarity   29.9%;   Pred. No. 1.2e+02;

RESULT 1450
ID   AAR58669 standard; protein; 476 AA.
DE   Human PACAP receptor type 1B mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE) TAKEDA CHEM IND LTD.
     Query Match   5.7%;   Score 68.5;   DB 2;   Length 476;
     Best Local Similarity   29.9%;   Pred. No. 1.2e+02;

RESULT 1451
ID   ADN24160 standard; protein; 488 AA.
DE   Bacterial polypeptide #6813.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

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Query Match             5.7%;   Score 68.5;   DB 8;   Length 488;
Best Local Similarity  22.4%;   Pred. No. 1.2e+02;
RESULT 1452
ID   ABP65829 standard; protein; 495 AA.
DE   Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:573.
PN   BP1227152-A1.
PD   31-JUL-2002.
PA   (NEST ) SOC PROD NESTLE SA.
Query Match             5.7%;   Score 68.5;   DB 5;   Length 495;
Best Local Similarity  28.6%;   Pred. No. 1.3e+02;
RESULT 1453
ID   AAB68618 standard; protein; 524 AA.
DE   Human PAC 1 receptor.
PN   WO20010747B-A1.
PD   01-FEB-2001.
PA   (MEDI-) MEDICAL RES COUNCIL.
Query Match             5.7%;   Score 68.5;   DB 4;   Length 524;
Best Local Similarity  29.9%;   Pred. No. 1.4e+02;
RESULT 1454
ID   AAR58659 standard; protein; 525 AA.
DE   Human PACAP receptor type 1A protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match             5.7%;   Score 68.5;   DB 2;   Length 525;
Best Local Similarity  29.9%;   Pred. No. 1.4e+02;
RESULT 1455
ID   ABU08611 standard; protein; 525 AA.
DE   Human pituitary adenylate cyclase (PAC) 1 receptor.
PN   US2002182729-A1.
PD   05-DEC-2002.
PA   (DICI/) DICICCO-BLOOM E.
PA   (NICO/) NICOT A.
PA   (LUNN/) LU N.
PA   (SUHJ/) SUH J.
Query Match             5.7%;   Score 68.5;   DB 6;   Length 525;
Best Local Similarity  29.9%;   Pred. No. 1.4e+02;
RESULT 1456
ID   ABP81873 standard; protein; 525 AA.
DE   Human PACAP receptor type 1 protein SEQ ID NO:231.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match             5.7%;   Score 68.5;   DB 6;   Length 525;
Best Local Similarity  29.9%;   Pred. No. 1.4e+02;
RESULT 1457
ID   ADN38958 standard; protein; 525 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:276.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match             5.7%;   Score 68.5;   DB 7;   Length 525;
Best Local Similarity  29.9%;   Pred. No. 1.4e+02;
RESULT 1458
ID   ABP73995 standard; protein; 541 AA.
DE   Candida albicans essential protein SEQ ID NO 7832.
PN   WO200253728-A2.
PD   11-JUL-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match             5.7%;   Score 68.5;   DB 5;   Length 541;
Best Local Similarity  21.7%;   Pred. No. 1.4e+02;
RESULT 1459
ID   ABG95329 standard; protein; 548 AA.
DE   Human novel secreted protein #150.
PN   US6420526-B1.
PD   16-JUL-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match             5.7%;   Score 68.5;   DB 5;   Length 548;
Best Local Similarity  34.0%;   Pred. No. 1.5e+02;
RESULT 1460
ID   ABO34523 standard; protein; 548 AA.
DE   Region of human secreted protein encoded by cDNA sequence #150.
PN   US2003049618-A1.
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PD   13-MAR-2003.
PA   (RUBE/) RUBEN S M.
PA   (ROSE/) ROSEN C A.
PA   (SOPP/) SOPPET D R.
PA   (CART/) CARTER K C.
PA   (BEDN/) BEDNARIK D P.
PA   (ENDR/) ENDRESS G A.
PA   (YUGG/) YU G.
PA   (NIUJ/) NI J.
PA   (FENG/) FENG P.
PA   (YOUN/) YOUNG P E.
PA   (GREE/) GREENE J M.
PA   (FERR/) FERRIE A M.
PA   (DUAN/) DUAN D R.
PA   (HUUJ/) HU J.
PA   (FLOR/) FLORENCE K A.
PA   (OLSE/) OLSEN H S.
PA   (FISC/) FISCHER C L.
PA   (EBNE/) EBNER R.
PA   (BREW/) BREWER L A.
PA   (MOOR/) MOORE P A.
PA   (SHIY/) SHI Y.
PA   (LAFL/) LAFLEUR D W.
PA   (LIYY/) LI Y.
PA   (ZENG/) ZENG Z.
PA   (KYAW/) KYAW H.
Query Match             5.7%;   Score 68.5;   DB 6;   Length 548;
Best Local Similarity  34.0%;   Pred. No. 1.5e+02;
RESULT 1461
ID   ADI23184 standard; protein; 548 AA.
DE   Novel human secreted protein seq id 469.
PN   US2003175858-A1.
PD   18-SEP-2003.
PA   (RUBE/) RUBEN S M.
PA   (ROSE/) ROSEN C A.
PA   (SOPP/) SOPPET D R.
PA   (CART/) CARTER K C.
PA   (BEDN/) BEDNARIK D P.
PA   (ENDR/) ENDRESS G A.
PA   (YUGG/) YU G.
PA   (NIUJ/) NI J.
PA   (FENG/) FENG P.
PA   (YOUN/) YOUNG P E.
PA   (GREE/) GREENE J M.
PA   (FERR/) FERRIE A M.
PA   (DUAN/) DUAN D R.
PA   (HUUJ/) HU J.
PA   (FLOR/) FLORENCE K A.
PA   (OLSE/) OLSEN H S.
PA   (FISC/) FISCHER C L.
PA   (EBNE/) EBNER R.
PA   (BREW/) BREWER L A.
PA   (MOOR/) MOORE P A.
PA   (SHIY/) SHI Y.
PA   (LAFL/) LAFLEUR D W.
PA   (LIYY/) LI Y.
PA   (ZENG/) ZENG Z.
PA   (KYAW/) KYAW H.
Query Match             5.7%;   Score 68.5;   DB 7;   Length 548;
Best Local Similarity  34.0%;   Pred. No. 1.5e+02;
RESULT 1462
ID   ADH17089 standard; protein; 548 AA.
DE   Human translation initiation factor eIF3 p66 subunit protein.
PN   WO2003097854-A2.
PD   27-NOV-2003.
PA   (SUGE-) SUGEN INC.
Query Match             5.7%;   Score 68.5;   DB 8;   Length 548;
Best Local Similarity  34.0%;   Pred. No. 1.5e+02;
RESULT 1463
ID   ADH74186 standard; protein; 548 AA.
DE   Human secreted protein #150.
PN   US2003225248-A1.
PD   04-DEC-2003.
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PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match   5.7%; Score 68.5; DB 8; Length 548;
      Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1464
ID   ABM82346 standard; protein; 548 AA.
DE   Tumour-associated antigenic target (TAT) polypeptide PRO22481, SEQ:6028.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.
      Query Match   5.7%; Score 68.5; DB 8; Length 548;
      Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1465
ID   AAR58661 standard; protein; 552 AA.
DE   Human PACAP receptor type 1-B2 protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.7%; Score 68.5; DB 2; Length 552;
      Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1466
ID   AAR58662 standard; protein; 553 AA.
DE   Human PACAP receptor type 1C protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.7%; Score 68.5; DB 2; Length 553;
      Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1467
ID   AAR58660 standard; protein; 553 AA.
DE   Human PACAP receptor type 1B protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.7%; Score 68.5; DB 2; Length 553;
      Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1468
ID   ABB11705 standard; peptide; 588 AA.
DE   Human GABA transporter homologue, SEQ ID NO:2075.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
      Query Match   5.7%; Score 68.5; DB 4; Length 588;
      Best Local Similarity 19.6%; Pred. No. 1.6e+02;
RESULT 1469
ID   ADP98892 standard; protein; 597 AA.
DE   C. albicans specific gene, orf6.4254, protein sequence.
PN   WO200405965-A2.
PD   08-JUL-2004.
PA   (ELIT-) ELITRA PHARM INC.
PA   (ELIT-) ELITRA CANADA LTD.
      Query Match   5.7%; Score 68.5; DB 8; Length 597;
      Best Local Similarity 26.2%; Pred. No. 1.6e+02;
RESULT 1470
ID   ADS10834 standard; protein; 600 AA.
DE   Human therapeutic protein - SEQ ID 1071.
PN   WO200408148-A2.
PD   23-SEP-2004.
PA   (NUVE-) NUVELO INC.
      Query Match   5.7%; Score 68.5; DB 8; Length 600;
      Best Local Similarity 19.6%; Pred. No. 1.6e+02;
RESULT 1471
ID   ABU38306 standard; protein; 634 AA.
DE   Protein encoded by Prokaryotic essential gene #23833.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   5.7%; Score 68.5; DB 6; Length 634;
      Best Local Similarity 26.3%; Pred. No. 1.8e+02;
RESULT 1472
ID   ABO81139 standard; protein; 660 AA.
DE   Pseudomonas aeruginosa polypeptide #13314.
PN   US6551795-B1.
PD   22-APR-2003.

PA   (GENO-) GENOME THERAPEUTICS CORP.
      Query Match   5.7%; Score 68.5; DB 7; Length 660;
      Best Local Similarity 26.3%; Pred. No. 1.9e+02;
RESULT 1473
ID   AAG20246 standard; protein; 663 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 22359.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (GETH) GENENTECH INC.
      Query Match   5.7%; Score 68.5; DB 3; Length 663;
      Best Local Similarity 22.3%; Pred. No. 1.9e+02;
RESULT 1474
ID   ABB53933 standard; protein; 670 AA.
DE   Lactococcus lactis protein kup1.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
      Query Match   5.7%; Score 68.5; DB 5; Length 670;
      Best Local Similarity 22.1%; Pred. No. 1.9e+02;
RESULT 1475
ID   ABU50927 standard; protein; 691 AA.
DE   Helicobacter pylori selected interacting domain (SID) protein #270.
PN   WO200266501-A2.
PD   29-AUG-2002.
PA   (HYBR-) HYBRIGENICS.
PA   (INSP) INST PASTEUR.
      Query Match   5.7%; Score 68.5; DB 5; Length 691;
      Best Local Similarity 19.2%; Pred. No. 2e+02;
RESULT 1476
ID   AAG20245 standard; protein; 704 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 22358.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (GETH) GENENTECH INC.
      Query Match   5.7%; Score 68.5; DB 3; Length 704;
      Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1477
ID   AAG20244 standard; protein; 724 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 22357.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (CROP-) CROPDESIGN NV.
      Query Match   5.7%; Score 68.5; DB 3; Length 724;
      Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1478
ID   AAU72535 standard; protein; 724 AA.
DE   Arabidopsis cell cycle protein CCP25.
PN   WO20018946-A2.
PD   15-NOV-2001.
PA   (CROP-) CROPDESIGN NV.
      Query Match   5.7%; Score 68.5; DB 5; Length 724;
      Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1479
ID   ADS23914 standard; protein; 731 AA.
DE   Bacterial polypeptide #12947.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
      Query Match   5.7%; Score 68.5; DB 8; Length 731;
      Best Local Similarity 25.9%; Pred. No. 2.2e+02;
RESULT 1480
ID   ADC95469 standard; protein; 738 AA.
DE   E. faecium protein sequence SEQ ID 5096.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
      Query Match   5.7%; Score 68.5; DB 7; Length 738;
      Best Local Similarity 20.3%; Pred. No. 2.2e+02;
RESULT 1481
ID   AAB46310 standard; protein; 788 AA.
DE   H. pylori HPS115 protein.
PN   WO200073352-A2.

```
PD   07-DEC-2000.
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA   (CREA-) CREATOGEN GMBH.
     Query Match             5.7%;  Score 68.5;  DB 4;  Length 788;
     Best Local Similarity   19.2%;  Pred. No. 2.4e+02;
RESULT 1482
ID   AAY92103 standard; protein; 885 AA.
DE   Human WFS1 mutant DEL508 YVVLL.
PN   WO200018787-A1.
PD   06-APR-2000.
PA   (UNIW ) UNIV WASHINGTON.
PA   (PERM/) PERMUTT M A.
PA   (INOU/) INOUE H.
PA   (MUEC/) MUECKLER M.
     Query Match             5.7%;  Score 68.5;  DB 3;  Length 885;
     Best Local Similarity   23.8%;  Pred. No. 2.8e+02;
RESULT 1483
ID   AAY92105 standard; protein; 890 AA.
DE   Human WFS1 mutant G695V.
PN   WO200018787-A1.
PD   06-APR-2000.
PA   (UNIW ) UNIV WASHINGTON.
PA   (PERM/) PERMUTT M A.
PA   (INOU/) INOUE H.
PA   (MUEC/) MUECKLER M.
     Query Match             5.7%;  Score 68.5;  DB 3;  Length 890;
     Best Local Similarity   23.8%;  Pred. No. 2.9e+02;
RESULT 1484
ID   AAY92107 standard; protein; 890 AA.
DE   Human WFS1 mutant P504L.
PN   WO200018787-A1.
PD   06-APR-2000.
PA   (UNIW ) UNIV WASHINGTON.
PA   (PERM/) PERMUTT M A.
PA   (INOU/) INOUE H.
PA   (MUEC/) MUECKLER M.
     Query Match             5.7%;  Score 68.5;  DB 3;  Length 890;
     Best Local Similarity   23.8%;  Pred. No. 2.9e+02;
RESULT 1485
ID   AAY92110 standard; protein; 890 AA.
DE   Human WFS1 polymorphism I333V.
PN   WO200018787-A1.
PD   06-APR-2000.
PA   (UNIW ) UNIV WASHINGTON.
PA   (PERM/) PERMUTT M A.
PA   (INOU/) INOUE H.
PA   (MUEC/) MUECKLER M.
     Query Match             5.7%;  Score 68.5;  DB 3;  Length 890;
     Best Local Similarity   23.8%;  Pred. No. 2.9e+02;
RESULT 1486
ID   AAY92109 standard; protein; 890 AA.
DE   Human WFS1 polymorphism R456H.
PN   WO200018787-A1.
PD   06-APR-2000.
PA   (UNIW ) UNIV WASHINGTON.
PA   (PERM/) PERMUTT M A.
PA   (INOU/) INOUE H.
PA   (MUEC/) MUECKLER M.
     Query Match             5.7%;  Score 68.5;  DB 3;  Length 890;
     Best Local Similarity   23.8%;  Pred. No. 2.9e+02;
RESULT 1487
ID   AAY92100 standard; protein; 890 AA.
DE   WFS1 polypeptide.
PN   WO200018787-A1.
PD   06-APR-2000.
PA   (UNIW ) UNIV WASHINGTON.
PA   (PERM/) PERMUTT M A.
PA   (INOU/) INOUE H.
PA   (MUEC/) MUECKLER M.
     Query Match             5.7%;  Score 68.5;  DB 3;  Length 890;
     Best Local Similarity   23.8%;  Pred. No. 2.9e+02;
RESULT 1488
ID   AAY92104 standard; protein; 890 AA.

DE   Human WFS1 mutant P724L.
PN   WO200018787-A1.
PD   06-APR-2000.
PA   (UNIW ) UNIV WASHINGTON.
PA   (PERM/) PERMUTT M A.
PA   (INOU/) INOUE H.
PA   (MUEC/) MUECKLER M.
     Query Match             5.7%;  Score 68.5;  DB 3;  Length 890;
     Best Local Similarity   23.8%;  Pred. No. 2.9e+02;
RESULT 1489
ID   ABP29861 standard; protein; 894 AA.
DE   Streptococcus polypeptide SEQ ID NO 8898.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match             5.7%;  Score 68.5;  DB 5;  Length 894;
     Best Local Similarity   22.9%;  Pred. No. 2.9e+02;
RESULT 1490
ID   ABP28153 standard; protein; 894 AA.
DE   Streptococcus polypeptide SEQ ID NO 5482.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match             5.7%;  Score 68.5;  DB 5;  Length 894;
     Best Local Similarity   22.9%;  Pred. No. 2.9e+02;
RESULT 1491
ID   AAY92102 standard; protein; 937 AA.
DE   Human WFS1 mutant del88fs/ter937.
PN   WO200018787-A1.
PD   06-APR-2000.
PA   (UNIW ) UNIV WASHINGTON.
PA   (PERM/) PERMUTT M A.
PA   (INOU/) INOUE H.
PA   (MUEC/) MUECKLER M.
     Query Match             5.7%;  Score 68.5;  DB 3;  Length 937;
     Best Local Similarity   23.8%;  Pred. No. 3.1e+02;
RESULT 1492
ID   ADN19015 standard; protein; 1004 AA.
DE   Bacterial polypeptide #1668.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match             5.7%;  Score 68.5;  DB 8;  Length 1004;
     Best Local Similarity   19.6%;  Pred. No. 3.4e+02;
RESULT 1493
ID   ADB70303 standard; protein; 1178 AA.
DE   C. neoformans amino acid sequence SEQ ID NO:3347.
PN   WO2003052076-A2.
PD   26-JUN-2003.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             5.7%;  Score 68.5;  DB 7;  Length 1178;
     Best Local Similarity   19.8%;  Pred. No. 4.2e+02;
RESULT 1494
ID   AAW88448 standard; protein; 1296 AA.
DE   Caenorhabditis elegans NPC1 protein orthologue.
PN   WO9901555-A1.
PD   14-JAN-1999.
PA   (USSH ) US DEPT HEALTH & HUMAN RESOURCES.
     Query Match             5.7%;  Score 68.5;  DB 2;  Length 1296;
     Best Local Similarity   25.8%;  Pred. No. 4.8e+02;
RESULT 1495
ID   AAB30730 standard; protein; 3015 AA.
DE   Amino acid sequence of chimeric Hepatitis C virus clone pH77CV-J6S.
PN   WO200075338-A2.
PD   14-DEC-2000.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
     Query Match             5.7%;  Score 68.5;  DB 4;  Length 3015;
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       Best Local Similarity    26.7%;   Pred. No. 1.5e+03;
RESULT 1496
ID    AAB30732 standard; protein; 3015 AA.
DE    Amino acid sequence of chimeric Hepatitis C virus clone J6S.
PN    WO20007533B-A2.
PD    14-DEC-2000.
PA    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
       Query Match               5.7%;   Score 68.5;   DB 4;   Length 3015;
       Best Local Similarity    26.7%;   Pred. No. 1.5e+03;
RESULT 1497
ID    ADK16845 standard; protein; 200 AA.
DE    Nanoarchaeum equitans cancer-associated (CA) protein #398.
PN    WO2003093434-A2.
PD    13-NOV-2003.
PA    (DIVE-) DIVERSA CORP.
       Query Match               5.7%;   Score 68;   DB 8;   Length 200;
       Best Local Similarity    23.5%;   Pred. No. 41;
RESULT 1498
ID    AAB78946 standard; protein; 247 AA.
DE    C. glutamicum SRT protein sequence SEQ ID NO:152.
PN    WO200100804-A2.
PD    04-JAN-2001.
PA    (BADI ) BASF AG.
       Query Match               5.7%;   Score 68;   DB 4;   Length 247;
       Best Local Similarity    23.1%;   Pred. No. 55;
RESULT 1499
ID    AAG91355 standard; protein; 247 AA.
DE    C glutamicum protein fragment SEQ ID NO: 5109.
PN    EP1108790-A2.
PD    20-JUN-2001.
PA    (KYOW ) KYOWA HAKKO KOGYO KK.
       Query Match               5.7%;   Score 68;   DB 4;   Length 247;
       Best Local Similarity    23.1%;   Pred. No. 55;
RESULT 1500
ID    AAY41212 standard; protein; 258 AA.
DE    E. coli MttB polypeptide.
PN    WO9951753-A1.
PD    14-OCT-1999.
PA    (UYAL-) UNIV ALBERTA.
       Query Match               5.7%;   Score 68;   DB 2;   Length 258;
       Best Local Similarity    23.0%;   Pred. No. 59;
```

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 16, 2005, 21:31:27 ; Search time 16 Seconds
            (without alignments)
            1407.170 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSQSSHA.........EAGSBEAEEKQDSEKPLLEL 234

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1500 summaries

Database :   PIR 79:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	664	55.6	445	2	I38027	MLN 64 protein - h
2	204	17.1	478	2	T16170	hypothetical prote
3	102.5	8.6	348	2	H90281	hypothetical prote
4	93.5	7.8	424	2	D75080	glucose-1-phosphat
5	90	7.5	1911	2	T43048	calcium channel al
6	86.5	7.2	767	2	T21969	hypothetical prote
7	85.5	7.2	396	2	B81299	probable molybdopt
8	85.5	7.2	438	2	A57219	Batten disease-rel
9	85	7.1	448	2	G70172	conserved hypothet
10	84.5	7.1	471	2	A41680	integral membrane
11	83.5	7.0	352	2	H97002	probable integral
12	83	6.9	291	2	AE0302	sugar ABC transpor
13	83	6.9	590	1	S34960	NADH2 dehydrogenas
14	82.5	6.9	186	2	B29835	TraS protein - Esc
15	82.5	6.9	239	1	C64227	hypothetical prote
16	82.5	6.9	341	2	S51265	probable N-acetylg
17	82.5	6.9	406	2	T43120	conserved hypothet
18	82.5	6.9	891	2	T37397	major core protein
19	82	6.9	589	2	T52070	RNA1 protein homol
20	82	6.9	589	2	A36983	RNA1 homolog fug1
21	82	6.9	1466	2	T30566	ATP-binding casset
22	81	6.8	385	2	B4447	hypothetical prote
23	81	6.8	529	2	T23190	hypothetical prote
24	81	6.8	532	2	S46831	probable membrane
25	80.5	6.7	156	2	I84498	melatonin receptor
26	80.5	6.7	322	2	T45568	hypothetical prote
27	80.5	6.7	396	2	T50229	probable transmemb
28	80.5	6.7	417	2	C44038	tryptophan permeas
29	80.5	6.7	463	2	AE1155	amino acid transpo
30	80.5	6.7	536	2	A71491	probable integral
31	80.5	6.7	644	2	S63056	probable membrane
32	80.5	6.7	738	2	S10659	membrane protein t
33	80.5	6.7	891	1	WMVZ3S	major core protein
34	80.5	6.7	891	1	WMVZ3W	major core protein
35	80.5	6.7	1780	2	A85045	probable glucan sy
36	80	6.7	103	2	G75513	conserved hypothet
37	80	6.7	290	2	D89898	hypothetical prote
38	80	6.7	309	2	S59140	RTM1 protein - yea
39	80	6.7	388	2	H71115	hypothetical prote
40	80	6.7	1339	2	A84683	probable SNF2 subf
41	79.5	6.7	463	2	AH1513	amino acid transpo
42	79.5	6.7	491	1	EDBEIC	immediate-early pr
43	78.5	6.6	239	2	S73812	hypothetical prote
44	78.5	6.6	269	2	AF1532	spermidine/putresc
45	78.5	6.6	358	2	F64136	rnfD protein homol
46	78.5	6.6	471	2	S11280	serotonin receptor
47	78.5	6.6	678	2	S44925	IB3/5-polypeptide
48	78	6.5	245	2	JC5346	cdd2 protein - Clo
49	78	6.5	259	2	F83825	hypothetical prote
50	78	6.5	382	2	E97157	stage III sporulat
51	78	6.5	471	2	B64099	undecaprenyl-phosp
52	78	6.5	1297	2	T39287	hypothetical prote
53	78	6.5	2136	2	A05037	hypothetical prote
54	77.5	6.5	269	2	AH1175	spermidine/putresc
55	77.5	6.5	299	2	AE0461	probable membrane
56	77.5	6.5	327	2	F82904	conserved hypothet
57	77.5	6.5	328	2	F84130	ABC transporter (p
58	77.5	6.5	338	2	T39159	hypothetical prote
59	77.5	6.5	440	2	T11319	NADH2 dehydrogenas
60	77.5	6.5	491	2	B69499	sodium- and chlori
61	77.5	6.5	512	2	AC3399	probable colanic b
62	77.5	6.5	734	1	DERZN5	NADH2 dehydrogenas
63	77.5	6.5	892	2	H72164	A1lL protein - var
64	77.5	6.5	892	2	T28552	hypothetical prote
65	77.5	6.5	892	2	B36849	AiOL protein - var
66	77.5	6.5	1784	2	T43167	sodium channel pro
67	77	6.4	332	2	T23307	hypothetical prote
68	77	6.4	559	2	C87307	hypothetical prote
69	77	6.4	590	1	QQUTC5	NADH2 dehydrogenas
70	77	6.4	650	2	A90072	hypothetical prote
71	77	6.4	991	2	TO1377	hypothetical prote
72	77	6.4	1025	2	T18376	multidrug resistan
73	77	6.4	1117	2	C85018	hypothetical prote
74	77	6.4	1500	2	G84922	hypothetical prote
75	76.5	6.4	278	2	B85807	probable tail fibe
76	76.5	6.4	278	2	H90958	phage tail protein
77	76.5	6.4	282	2	H95869	probable sugar ABC
78	76.5	6.4	352	2	T25170	hypothetical prote
79	76.5	6.4	352	2	AF0692	probable membrane
80	76.5	6.4	494	2	JC5919	potassium channel
81	76.5	6.4	538	2	E81435	probable iron-upta
82	76.5	6.4	589	2	A71918	probable secretion
83	76.5	6.4	646	2	T41545	hypothetical trans
84	76	6.4	342	2	T11476	NADH2 dehydrogenas
85	76	6.4	402	2	T24184	hypothetical prote
86	76	6.4	669	2	T48466	NADH2 dehydrogenas
87	76	6.4	1402	2	T24664	hypothetical prote
88	76	6.4	1450	2	JC6139	cystic fibrosis tr
89	76	6.4	1783	2	T37258	probable voltage-d
90	76	6.4	1917	2	C88728	protein C48A7.1 [i
91	75.5	6.3	156	2	I62107	melatonin receptor
92	75.5	6.3	263	2	G95198	hypothetical prote
93	75.5	6.3	263	2	C98065	hypothetical prote
94	75.5	6.3	339	2	B82211	conserved hypothet
95	75.5	6.3	352	2	H64919	probable membrane
96	75.5	6.3	352	2	G85769	hypothetical prote
97	75.5	6.3	352	2	C90921	hypothetical prote
98	75.5	6.3	415	2	F91209	melatonin receptor
99	75.5	6.3	415	2	A86056	low affinity trypt
100	75.5	6.3	415	2	A39412	low affinity trypt
101	75.5	6.3	471	2	S40689	tryptophan transpo
102	75.5	6.3	498	2	T11039	5-hydroxytryptamin

#			Len		Accession	Description
103	75.5	6.3	593	2	H64594	multidrug resistan
104	75.5	6.3	708	2	T29669	hypothetical prote
105	75.5	6.3	775	2	T52107	anion channel prot
106	75.5	6.3	1142	2	T39103	probable negative
107	75	6.3	249	2	G64470	sulfate/thiosulfat
108	75	6.3	274	2	A82509	probable phosphati
109	75	6.3	330	2	B71163	probable oligopept
110	75	6.3	473	2	A38627	gamma-aminobutyric
111	75	6.3	526	2	T45850	hypothetical prote
112	75	6.3	649	2	C69810	anion-binding prot
113	75	6.3	753	2	H90124	hypothetical prote
114	75	6.3	2248	1	D42088	adenylate cyclase
115	74.5	6.2	276	2	A95881	probable trehalose
116	74.5	6.2	335	2	H72420	oligopeptide ABC t
117	74.5	6.2	355	2	JC4304	orphan G protein-c
118	74.5	6.2	471	2	A34863	serotonin receptor
119	74.5	6.2	473	2	B84143	Na+/H+ antiporter
120	74.5	6.2	500	1	T14826	transcription init
121	74.5	6.2	574	2	T05964	probable low-affin
122	74.5	6.2	618	1	S38004	probable transport
123	74.5	6.2	1808	2	T47792	hypothetical prote
124	74.5	6.2	231	1	C69540	cobalamin (5'-phos
125	74	6.2	231	2	B69422	quinone-reactive N
126	74	6.2	281	1	S26018	NADH2 dehydrogenas
127	74	6.2	286	2	S73424	spermidine/putresc
128	74	6.2	312	2	C72547	probable aspartate
129	74	6.2	312	2	H86732	hypothetical prote
130	74	6.2	349	2	JC6311	interferon recepto
131	74	6.2	350	2	I38848	Mel-1a melatonin r
132	74	6.2	396	2	H89869	hypothetical prote
133	74	6.2	442	2	C86859	transmembrane effl
134	74	6.2	449	2	S02011	serotonin receptor
135	74	6.2	475	2	T36137	probable amino aci
136	74	6.2	485	2	T24115	hypothetical prote
137	74	6.2	487	1	C71417	cytochrome P450 di
138	74	6.2	493	2	JC7378	L-lysine 6-aminotr
139	74	6.2	1123	2	T51517	telomerase reverse
140	73.5	6.2	153	2	B95845	conserved hypothet
141	73.5	6.2	192	2	A84727	hypothetical prote
142	73.5	6.2	216	2	G70474	hypothetical prote
143	73.5	6.2	318	2	S76713	hypothetical prote
144	73.5	6.2	338	2	I40448	conserved hypothet
145	73.5	6.2	379	2	S58448	ubiquinol-cytochro
146	73.5	6.2	384	2	AF0636	glucans biosynthes
147	73.5	6.2	385	1	S01511	ubiquinol-cytochro
148	73.5	6.2	385	2	A69804	ABC transporter (A
149	73.5	6.2	413	2	AD1738	Similar to multidr
150	73.5	6.2	442	2	C96672	hypothetical prote
151	73.5	6.2	491	1	EDBEM5	immediate-early pr
152	73.5	6.2	634	2	F82623	potassium uptake p
153	73.5	6.2	637	2	H83945	DNA mismatch repai
154	73.5	6.2	640	2	B32935	hexose transport p
155	73.5	6.2	731	2	T31914	hypothetical prote
156	73.5	6.2	1095	2	E96744	probable oligopept
157	73.5	6.2	1174	2	A39927	RNA-directed RNA p
158	73	6.1	114	2	F71925	cag island protein
159	73	6.1	282	2	S26030	NADH2 dehydrogenas
160	73	6.1	339	2	T15560	hypothetical prote
161	73	6.1	450	1	WZBEE4	49.2K membrane pro
162	73	6.1	453	2	T30985	hypothetical prote
163	73	6.1	553	2	A71823	hypothetical prote
164	73	6.1	788	2	G89901	hypothetical prote
165	73	6.1	971	2	T00268	hypothetical prote
166	73	6.1	1075	2	B96508	hypothetical prote
167	73	6.1	6805	2	S20901	titin - rabbit (fr
168	72.5	6.1	209	2	S72929	hypothetical prote
169	72.5	6.1	222	2	B85866	probable transport
170	72.5	6.1	222	2	B91022	probable transport
171	72.5	6.1	222	2	H64996	hypothetical prote
172	72.5	6.1	255	2	A60944	ubiquinol-cytochro
173	72.5	6.1	291	2	T02986	chlorophyll a/b-bi
174	72.5	6.1	307	2	A86696	conserved hypothet
175	72.5	6.1	315	2	H96598	protein F20N2.8 [i
176	72.5	6.1	325	2	H86670	hypothetical prote
177	72.5	6.1	336	2	C88951	protein C38C3.2 [i
178	72.5	6.1	389	2	A55493	oxytocin receptor
179	72.5	6.1	428	2	AF0173	probable paraquat-
180	72.5	6.1	499	2	H70453	virulence factor M
181	72.5	6.1	513	2	S47631	pituitary adenylat
182	72.5	6.1	522	2	T29705	hypothetical prote
183	72.5	6.1	635	2	T23465	hypothetical prote
184	72.5	6.1	718	2	S57913	probable transloca
185	72.5	6.1	749	2	C84508	probable cap-bindi
186	72.5	6.1	1539	2	T30037	hypothetical prote
187	72	6.0	279	2	T21099	hypothetical prote
188	72	6.0	306	2	AE1156	hypothetical prote
189	72	6.0	339	2	G97199	probable permease
190	72	6.0	377	2	T27805	hypothetical prote
191	72	6.0	379	2	T11349	ubiquinol-cytochro
192	72	6.0	415	1	WMAD52	late L1 52K protei
193	72	6.0	415	1	WMAD65	late L1 52K protei
194	72	6.0	453	2	T39155	glycosyl hydrolase
195	72	6.0	453	2	D89760	conserved hypothet
196	72	6.0	479	2	S64587	hypothetical prote
197	72	6.0	497	2	G96611	probable cytochrom
198	72	6.0	514	2	T15338	hypothetical prote
199	72	6.0	594	2	T42660	hypothetical prote
200	72	6.0	600	2	T39873	hypothetical prote
201	72	6.0	630	2	T07966	probable ethylene
202	72	6.0	1038	2	S37854	hypothetical prote
203	72	6.0	1094	2	S22573	DNA-directed DNA p
204	72	6.0	1113	2	T20140	hypothetical prote
205	72	6.0	1220	2	T18291	patched protein -
206	72	6.0	1275	2	JU0092	trp protein - frui
207	72	6.0	1282	2	T30804	P-glycoprotein 6 -
208	71.5	6.0	210	2	S52050	cytochrome-c oxida
209	71.5	6.0	225	1	MMIH68	E1 membrane glycop
210	71.5	6.0	237	2	H70975	hypothetical prote
211	71.5	6.0	246	2	AG3644	flagellar biosynth
212	71.5	6.0	301	2	F86647	hypothetical prote
213	71.5	6.0	341	2	F90084	hypothetical prote
214	71.5	6.0	345	2	T33706	hypothetical prote
215	71.5	6.0	348	2	D82252	RnfD-related prote
216	71.5	6.0	355	2	AB3516	sensory transducti
217	71.5	6.0	362	2	S48689	prostaglandin E(2)
218	71.5	6.0	362	2	S51280	EP3-alpha receptor
219	71.5	6.0	366	2	I46469	Mel-1a melatonin r
220	71.5	6.0	381	2	T11776	ubiquinol-cytochro
221	71.5	6.0	383	2	T38194	hypothetical prote
222	71.5	6.0	386	1	S34043	oxytocin receptor
223	71.5	6.0	390	2	S66497	isotocin receptor
224	71.5	6.0	435	2	AD1340	maltodextrin ABC-t
225	71.5	6.0	435	2	AB1711	maltodextrin ABC-t
226	71.5	6.0	471	2	PS0154	125K surface antig
227	71.5	6.0	510	2	T10124	hexose transport p
228	71.5	6.0	524	2	T02499	hypothetical prote
229	71.5	6.0	603	2	H90061	hypothetical prote
230	71.5	6.0	651	2	T46050	hypothetical prote
231	71.5	6.0	669	2	D64137	betT protein homol
232	71.5	6.0	670	2	A49580	mediates transport
233	71.5	6.0	823	2	T34472	hypothetical prote
234	71.5	6.0	1407	2	B42239	adenylate cyclase
235	71.5	6.0	3010	1	S18030	genome polyprotein
236	71	5.9	114	2	H64586	cag pathogenicity
237	71	5.9	225	1	MMIHAI	E1 membrane glycop
238	71	5.9	250	2	A82367	conserved hypothet
239	71	5.9	258	2	A81355	probable processin
240	71	5.9	290	2	S33443	chlorophyll a/b-bi
241	71	5.9	339	2	T16745	hypothetical prote
242	71	5.9	345	2	T12372	NADH2 dehydrogenas
243	71	5.9	345	2	T25561	hypothetical prote
244	71	5.9	361	2	C90603	hypothetical prote
245	71	5.9	391	2	F86759	hypothetical prote
246	71	5.9	416	2	E87286	3-deoxy-D-manno-oc
247	71	5.9	423	2	AF1335	transcription regu
248	71	5.9	471	2	A43956	serotonin receptor

#	%	%	Accession	n	Length	Description
249	71	5.9	S48932	2	546	hypothetical prote
250	71	5.9	T38766	2	563	probable transcrip
251	71	5.9	T22509	2	576	hypothetical prote
252	71	5.9	A58932	2	620	cytochrome C-type
253	71	5.9	E96725	2	676	hypothetical prote
254	71	5.9	E71813	2	788	probable component
255	71	5.9	T52485	2	913	neurofilament prot
256	71	5.9	T18482	2	2437	hypothetical prote
257	70.5	5.9	T31684	1	203	hypothetical prote
258	70.5	5.9	H98208	2	266	probable bacitraci
259	70.5	5.9	AI3077	2	266	probable permease
260	70.5	5.9	T41414	2	266	hypothetical prote
261	70.5	5.9	AH2408	2	279	probable receptor-
262	70.5	5.9	S22041	2	291	permease protein o
263	70.5	5.9	S76294	2	340	hypothetical prote
264	70.5	5.9	B90537	2	352	hypothetical prote
265	70.5	5.9	I38748	2	365	protaglandin recep
266	70.5	5.9	S51315	2	365	protaglandin E re
267	70.5	5.9	I38747	2	374	protaglandin recep
268	70.5	5.9	S51317	2	374	prostaglandin E re
269	70.5	5.9	S51316	2	388	prostaglandin E re
270	70.5	5.9	I38750	2	388	protaglandin recep
271	70.5	5.9	S71336	2	389	mesotocin receptor
272	70.5	5.9	S43375	2	390	prostaglandin E re
273	70.5	5.9	S51313	2	390	prostaglandin E re
274	70.5	5.9	S51318	2	393	prostaglandin E re
275	70.5	5.9	E71065	2	423	prostaglandin E re
276	70.5	5.9	S51319	2	425	prostaglandin E re
277	70.5	5.9	AG3600	2	472	cellulose synthase
278	70.5	5.9	B64638	2	496	conserved hypothet
279	70.5	5.9	B64181	2	521	probable cytochrom
280	70.5	5.9	A81650	2	548	conserved hypothet
281	70.5	5.9	T16790	2	556	hypothetical prote
282	70.5	5.9	S45754	2	574	probable membrane
283	70.5	5.9	F46027	2	598	gamma-aminobutyric
284	70.5	5.9	ACRTGT	1	599	gamma-aminobutyric
285	70.5	5.9	T10566	2	700	probable serine/th
286	70.5	5.9	T48463	2	766	hypothetical prote
287	70.5	5.9	T18220	2	1026	chitin synthase (E
288	70.5	5.9	F97846	2	1583	hypothetical prote
289	70.5	5.9	T20160	2	1787	hypothetical prote
290	70.5	5.9	B96695	2	5138	hypothetical prote
291	70	5.9	T51847	2	189	manganese-binding
292	70	5.9	T08902	2	199	manganese-binding
293	70	5.9	F86310	2	213	protein F1L3:8 [im
294	70	5.9	T13597	2	256	chlorophyll a/b-bi
295	70	5.9	T52317	2	287	H+-transporting tw
296	70	5.9	H64244	2	292	ABC transporter, p
297	70	5.9	B95010	2	307	hypothetical prote
298	70	5.9	B97882	2	307	hypothetical prote
299	70	5.9	T30981	2	330	G protein-coupled
300	70	5.9	I38974	2	333	hypothetical prote
301	70	5.9	T46421	2	371	oxytocin receptor
302	70	5.9	A55597	2	388	probable ankyrin-r
303	70	5.9	A85112	2	416	proline/betaine tr
304	70	5.9	T08882	2	418	sugar ABC transpor
305	70	5.9	E72357	2	420	hypothetical prote
306	70	5.9	T01905	2	427	glutamate-aspartat
307	70	5.9	C91261	2	437	glutamate-aspartat
308	70	5.9	G86101	2	437	ABC transporter, m
309	70	5.9	AF3215	2	438	envelope protein 5
310	70	5.9	T42595	2	450	related to COPI-in
311	70	5.9	B89827	2	494	probable cytochrom
312	70	5.9	T49467	2	532	hypothetical prote
313	70	5.9	A87019	2	551	hypothetical prote
314	70	5.9	T27878	2	554	hypothetical prote
315	70	5.9	H72565	2	558	hypothetical prote
316	70	5.9	T22323	2	675	urea transport pro
317	70	5.9	S46830	2	735	hypothetical prote
318	70	5.9	T26022	2	963	hypothetical prote
319	70	5.9	F86200	2	1930	protein F12K1.17
320	69.5	5.8	MNIHHC	1	133	nonstructural prot
321	69.5	5.8	S76279	2	206	hypothetical prote
322	69.5	5.8	F70194	2	285	hypothetical prote
323	69.5	5.8	S59388	2	321	probable membrane
324	69.5	5.8	A97736	2	339	hypothetical prote
325	69.5	5.8	G90404	2	347	hypothetical prote
326	69.5	5.8	I58186	2	354	probable G protein
327	69.5	5.8	A53216	2	361	prostaglandin E2 r
328	69.5	5.8	S36766	2	362	prostaglandin E2 r
329	69.5	5.8	S62758	2	384	prostaglandin E re
330	69.5	5.8	S36765	2	385	ubiquinol-cytochro
331	69.5	5.8	S36767	2	387	prostaglandin E re
332	69.5	5.8	T32561	2	394	prostaglandin E re
333	69.5	5.8	AG1208	2	400	hypothetical prote
334	69.5	5.8	S51791	2	402	cell-division prot
335	69.5	5.8	E90986	2	405	Drosophila translo
336	69.5	5.8	H85831	2	405	probable colanic a
337	69.5	5.8	G64971	2	405	probable colanic a
338	69.5	5.8	B53216	2	411	Putative colanic a
339	69.5	5.8	S36764	2	417	prostaglandin E2 r
340	69.5	5.8	G72300	2	421	prostaglandin E re
341	69.5	5.8	T44832	2	436	conserved hypothet
342	69.5	5.8	D98003	2	453	probable emulsan r
343	69.5	5.8	T25798	2	477	conserved hypothet
344	69.5	5.8	E82740	2	490	hypothetical prote
345	69.5	5.8	C86250	2	503	C4-dicarboxylate t
346	69.5	5.8	T50054	2	507	hypothetical prote
347	69.5	5.8	E86534	2	515	probable transport
348	69.5	5.8	G86581	2	547	ADP/ATP translocas
349	69.5	5.8	F72042	2	547	integral membrane
350	69.5	5.8	JW0089	2	557	integral membrane
351	69.5	5.8	AC2137	2	557	organic cation tra
352	69.5	5.8	B96776	2	570	ABC transporter AT
353	69.5	5.8	D97337	2	577	hypothetical prote
354	69.5	5.8	AG1412	2	577	mismatch repair pr
355	69.5	5.8	AF1708	2	579	DNA polymerase III
356	69.5	5.8	S11073	2	599	DNA polymerase III
357	69.5	5.8	T31042	2	604	gamma-aminobutyric
358	69.5	5.8	F84525	2	607	hypothetical prote
359	69.5	5.8	E84463	2	616	Mutator-like trans
360	69.5	5.8	S58824	2	877	Mutator-like trans
361	69.5	5.8	S46633	2	881	probable membrane
362	69.5	5.8	A59188	2	1704	probable membrane
363	69.5	5.8	S71363	2	1704	ATP-binding casset
364	69.5	5.8	JT0382	2	1778	probable ATP-bindi
365	69.5	5.8	I46569	2	2629	apolipoprotein B -
366	69.5	5.8	T15789	2	7829	apolipoprotein B -
367	69	5.8	E83941	2	169	hypothetical prote
368	69	5.8	A96998	2	195	hypothetical prote
369	69	5.8	H96934	2	244	uncharacterized me
370	69	5.8	C64145	2	256	CDP-diglyceride sy
371	69	5.8	T07481	2	261	hypothetical prote
372	69	5.8	F83805	2	273	hypothetical prote
373	69	5.8	C71707	2	273	hypothetical prote
374	69	5.8	S72554	2	289	melatonin receptor
375	69	5.8	D96002	2	291	probable sugar upt
376	69	5.8	T32702	2	300	hypothetical prote
377	69	5.8	A99979	2	338	hypothetical prote
378	69	5.8	B69436	2	339	LSU ribosomal prot
379	69	5.8	AH1514	2	345	hypothetical prote
380	69	5.8	AD0273	2	351	probable integral
381	69	5.8	A58447	2	379	ubiquinol-cytochro
382	69	5.8	AI3175	2	382	conserved hypothet
383	69	5.8	D71424	2	383	hypothetical prote
384	69	5.8	I69644	2	388	O-antigen polymera
385	69	5.8	T11268	2	436	NADH2 dehydrogenas
386	69	5.8	A42384	2	437	glutamate-aspartat
387	69	5.8	T19512	2	443	hypothetical prote
388	69	5.8	S25821	2	478	transposase - Baci
389	69	5.8	T33985	2	478	hypothetical prote
390	69	5.8	B96804	2	508	probable thioredox
391	69	5.8	T11916	2	523	NADH2 dehydrogenas
392	69	5.8	T24675	2	540	hypothetical prote
393	69	5.8	E70784	2	549	cytochrome b homol
394	69	5.8	A64100	2	579	inner membrane cop

No.	%		Len	Accession	N	Description
395	69	5.8	599	G90476	2	probable Na+/H+ an
396	69	5.8	600	T11889	2	NADH2 dehydrogenas
397	69	5.8	637	H96592	2	probable multispan
398	69	5.8	659	D84613	2	probable multispan
399	69	5.8	791	T12455	2	hypothetical prote
400	69	5.8	802	JH0595	2	potassium channel
401	69	5.8	863	H84490	2	hypothetical prote
402	69	5.8	933	AD3309	2	hypothetical membr
403	69	5.8	1058	T30580	2	P-type ATPase - sl
404	69	5.8	1344	T34188	2	myb-binding protei
405	69	5.8	1392	T01908	2	hypothetical prote
406	69	5.8	1515	T04204	2	hypothetical prote
407	69	5.8	3010	A45573	1	genome polyprotein
408	68.5	5.7	225	AE0371	2	probable carboxype
409	68.5	5.7	237	T25877	2	hypothetical prote
410	68.5	5.7	238	T04280	2	hypothetical prote
411	68.5	5.7	260	H75428	2	hypothetical prote
412	68.5	5.7	262	AG1830	2	hypothetical prote
413	68.5	5.7	265	AI3428	2	hypothetical prote
414	68.5	5.7	285	E86835	2	maltose ABC transp
415	68.5	5.7	297	S74335	2	carbon dioxide con
416	68.5	5.7	304	AG3035	2	hypothetical prote
417	68.5	5.7	304	D98250	2	probable sugar ABC
418	68.5	5.7	343	AC2129	2	iron(III) dicitrat
419	68.5	5.7	359	B59105	2	hypothetical prote
420	68.5	5.7	362	D72424	2	oligopeptide ABC t
421	68.5	5.7	377	JQ2337	1	omega-3 fatty acid
422	68.5	5.7	383	I53870	2	Bdg-1 orphan recep
423	68.5	5.7	391	H81265	2	probable transmemb
424	68.5	5.7	395	B83774	2	hypothetical prote
425	68.5	5.7	395	A96189	2	hypothetical prote
426	68.5	5.7	395	AH3097	2	conserved hypothet
427	68.5	5.7	419	AG1660	2	multidrug resistan
428	68.5	5.7	420	I51666	2	Mel-1c receptor su
429	68.5	5.7	425	F97108	2	probable glycosylt
430	68.5	5.7	430	S15308	2	hypothetical prote
431	68.5	5.7	431	H72247	2	preprotein translo
432	68.5	5.7	444	A48260	2	corticoliberin rec
433	68.5	5.7	445	E22845	2	hypothetical prote
434	68.5	5.7	479	T44326	2	hypothetical prote
435	68.5	5.7	480	B70446	2	hypothetical prote
436	68.5	5.7	488	T15941	2	hypothetical prote
437	68.5	5.7	492	G90574	2	hypothetical prote
438	68.5	5.7	502	S77331	2	NADH2 dehydrogenas
439	68.5	5.7	512	T00605	2	probable cytochrom
440	68.5	5.7	518	S50465	2	PAC2 protein - yea
441	68.5	5.7	525	JN0902	2	pituitary adenylat
442	68.5	5.7	542	S58102	2	hypothetical ,prote
443	68.5	5.7	558	F64235	2	Na+ ATPase chain J
444	68.5	5.7	634	C83530	2	potassium uptake p
445	68.5	5.7	670	G86702	2	potassium uptake [
446	68.5	5.7	724	H86427	2	unknown protein [i
447	68.5	5.7	788	G64707	1	cation-transportin
448	68.5	5.7	923	MMBY7C	2	probable membrane
449	68.5	5.7	1004	S55353	1	probable copper-tr
450	68	5.7	146	H75201	2	hypothetical prote
451	68	5.7	205	A64373	2	chemokine (C-C) re
452	68	5.7	255	F39925	2	ubiquinol-cytochro
453	68	5.7	266	C95316	2	prostaglandin E2 r
454	68	5.7	270	AB3627	2	hypothetical prote
455	68	5.7	279	AG2165	2	bicarbonate transp
456	68	5.7	294	T41953	2	G protein-coupled
457	68	5.7	294	AE0004	2	ribonuclease BN (E
458	68	5.7	313	B38888	2	COI intron 9 prote
459	68	5.7	355	A45177	2	chemokine (C-C) re
460	68	5.7	360	T11067	2	ubiquinol-cytochro
461	68	5.7	364	JC2115	2	prostaglandin E re
462	68	5.7	365	JN0693	2	prostaglandin E2 r
463	68	5.7	370	H90559	2	hypothetical prote
464	68	5.7	379	S58450	2	ubiquinol-cytochro
465	68	5.7	393	AG0184	2	probable multidrug
466	68	5.7	402	T41253	2	hypothetical wtf5
467	68	5.7	417	T11387	2	NADH2 dehydrogenas

No.	%		Len	Accession	N	Description
468	68	5.7	426	C69831	2	conserved hypothet
469	68	5.7	464	C70414	2	NADH2 dehydrogenas
470	68	5.7	473	H71044	2	cytochrome-c oxida
471	68	5.7	475	E83450	2	probable oxidoredu
472	68	5.7	477	H91123	2	probable oxidoredu
473	68	5.7	477	G85968	2	hypothetical 52.1
474	68	5.7	477	C65096	2	hypothetical prote
475	68	5.7	488	A53572	2	prostaglandin E2 r
476	68	5.7	502	I30010	1	NADH2 dehydrogenas
477	68	5.7	519	T39918	2	probable acetyl-co
478	68	5.7	542	A69261	2	probable acid-CoA
479	68	5.7	542	B81910	2	probable ABC-trans
480	68	5.7	542	B81105	2	ABC transporter. A
481	68	5.7	620	T19907	2	hypothetical prote
482	68	5.7	664	C84869	2	probable receptor
483	68	5.7	718	E83718	2	hypothetical prote
484	68	5.7	804	T49975	2	hypothetical prote
485	68	5.7	836	T18460	2	hypothetical prote
486	68	5.7	859	S69700	2	hypothetical prote
487	68	5.7	871	H72597	2	hypothetical prote
488	68	5.7	1429	T19422	2	hypothetical prote
489	68	5.7	1878	E86189	2	hypothetical prote
490	68	5.7	3010	GNWVTC	1	genome polyprotein
491	67.5	5.6	104	T36801	2	hypothetical prote
492	67.5	5.6	200	H72295	2	conserved hypothet
493	67.5	5.6	273	A97700	2	hypothetical prote
494	67.5	5.6	288	F72219	2	conserved hypothet
495	67.5	5.6	320	T23674	2	hypothetical prote
496	67.5	5.6	323	QQBED3	1	HHRF3 protein - hu
497	67.5	5.6	348	T12591	2	NADH2 dehydrogenas
498	67.5	5.6	354	T09353	2	G protein-coupled
499	67.5	5.6	362	C88086	2	protein T1IP1.1 [i
500	67.5	5.6	387	T24581	2	hypothetical prote
501	67.5	5.6	397	A83999	2	mutants block spor
502	67.5	5.6	419	AH1288	2	multidrug resistan
503	67.5	5.6	439	H83699	2	sodium-dependent c
504	67.5	5.6	450	G91219	2	TDP-Fuc4NAc lipidI
505	67.5	5.6	450	A86066	2	TDP-Fuc4NAc lipidI
506	67.5	5.6	450	F65183	2	4-alpha-l-fucosylt
507	67.5	5.6	452	G89870	2	vasoactive intesti
508	67.5	5.6	459	JH0594	2	hypothetical prote
509	67.5	5.6	483	G84113	2	NADH2 dehydrogenas
510	67.5	5.6	488	QXASM4	1	NADH2 dehydrogenas
511	67.5	5.6	492	F64464	2	sodium-dependent n
512	67.5	5.6	498	T48262	2	hypothetical prote
513	67.5	5.6	515	E72089	2	ADP, ATP carrier p
514	67.5	5.6	516	H82973	2	choline transporte
515	67.5	5.6	598	I51368	2	gamma-aminobutyric
516	67.5	5.6	632	A71259	2	probable dicarboxy
517	67.5	5.6	676	WZVZI8	1	I8 protein - vacci
518	67.5	5.6	676	T37345	2	NPH-II, helicase -
519	67.5	5.6	676	D42511	2	I8R protein - vacc
520	67.5	5.6	676	F36843	2	ATP/GTP-binding pr
521	67.5	5.6	676	T28500	2	hypothetical prote
522	67.5	5.6	682	D72158	2	L8R protein - vari
523	67.5	5.6	686	G82448	2	sensor histidine k
524	67.5	5.6	716	S30687	2	hypothetical prote
525	67.5	5.6	740	T02567	1	probable ATP-bindi
526	67.5	5.6	838	A54163	2	vacuolar ATPase (E
527	67.5	5.6	866	T20574	2	hypothetical prote
528	67.5	5.6	950	T15915	2	hypothetical prote
529	67.5	5.6	1159	T02866	2	hypothetical prote
530	67.5	5.6	1244	T19615	2	hypothetical prote
531	67.5	5.6	1411	S48442	2	PDR11 protein - ye
532	67.5	5.6	1753	S30855	2	hypothetical prote
533	67.5	5.6	2332	GNNYF	1	genome polyprotein
534	67	5.6	151	A72093	2	conserved hypothet
535	67	5.6	151	H86529	2	CT101 hypothetical
536	67	5.6	159	S61040	2	probable membrane
537	67	5.6	180	I48129	2	Xe169 (escapes X-i
538	67	5.6	203	D70150	1	hypothetical prote
539	67	5.6	225	MMIHIB	2	E1 membrane glycop
540	67	5.6	244	D70404	1	conserved hypothet

#			Description	Accession		Length
541	5.6	67	hypothetical prote	C90078	2	255
542	5.6	67	sugar ABC transpor	G98194	2	275
543	5.6	67	hypothetical prote	AC3092	2	275
544	5.6	67	hypothetical prote	S75698	2	275
545	5.6	67	conserved hypothet	F69307	2	276
546	5.6	67	DNA-damage repair	S35270	2	276
547	5.6	67	tRNA-processing ri	F96959	2	283
548	5.6	67	hypothetical prote	AE3024	2	285
549	5.6	67	hypothetical prote	D64235	2	286
550	5.6	67	hypothetical prote	D96703	2	314
551	5.6	67	inner membrane pro	D98260	2	317
552	5.6	67	ferrichrome transp	A96997	2	336
553	5.6	67	hypothetical prote	T21776	2	345
554	5.6	67	hypothetical prote	D84166	2	349
555	5.6	67	protein C50H1.2 [	C88987	2	350
556	5.6	67	hypothetical prote	T32314	2	352
557	5.6	67	ubiquinol-cytochro	S58451	2	379
558	5.6	67	ubiquinol-cytochro	S58449	2	379
559	5.6	67	pheromone shutdown	C69291	1	396
560	5.6	67	hypothetical prote	E70309	2	407
561	5.6	67	probable amino aci	B71500	2	411
562	5.6	67	pyruvate synthase	S74041	2	415
563	5.6	67	hypothetical prote	T46401	2	416
564	5.6	67	sodium-dependent t	C95085	2	423
565	5.6	67	proton glutamate s	AC1021	2	436
566	5.6	67	hypothetical prote	F86279	2	441
567	5.6	67	hypothetical prote	G72287	2	446
568	5.6	67	glucose transporte	A31986	2	496
569	5.6	67	glycine betaine tr	AB1707	2	507
570	5.6	67	ATP binding casset	AE0665	2	516
571	5.6	67	hypothetical prote	JC7777	2	646
572	5.6	67	dolichyl-phosphate	T49238	1	717
573	5.6	67	DNA topoisomerase	S58331	2	753
574	5.6	67	cell division prot	F81415	2	769
575	5.6	67	hypothetical prote	C82679	2	784
576	5.6	67	hypothetical prote	PN0677	2	787
577	5.6	67	probable serine/th	T34248	2	798
578	5.6	67	conserved hypothet	T05537	2	814
579	5.6	67	probable integral	T35280	2	823
580	5.6	67	conserved hypothet	D69427	2	880
581	5.6	67	probable NADH dehy	B82495	2	891
582	5.6	67	galactosamine-cont	B69631	2	900
583	5.6	67	chitin synthase (E	S39951	2	1175
584	5.6	67	DNA-directed DNA p	DJBEC1	1	1242
585	5.6	67	probable membrane	S63403	2	1333
586	5.6	67	pleiotropic drug r	A53151	2	1511
587	5.6	67	conserved hypothet	G82905	2	1575
588	5.6	67	hypothetical prote	T19481	2	1879
589	5.6	67	multidrug resistan	T18267	2	1905
590	5.6	67	sodium channel SCA	T30902	2	1993
591	5.6	67	genome polyprotein	GNWVCJ	1	3010
592	5.6	66.5	conserved hypothet	G69847	2	153
593	5.6	66.5	hypothetical prote	T28732	2	203
594	5.6	66.5	hypothetical prote	C70506	2	204
595	5.6	66.5	cag pathogenicity	C64586	2	218
596	5.6	66.5	sec-independant pr	A81405	2	245
597	5.6	66.5	hypothetical prote	AI2384	2	263
598	5.6	66.5	hypothetical prote	A70417	2	268
599	5.6	66.5	probable permease	AI0075	2	272
600	5.6	66.5	nitrate transport	S56642	1	279
601	5.6	66.5	conserved hypothet	E70322	2	279
602	5.6	66.5	sugar ABC transpor	A84110	2	293
603	5.6	66.5	hypothetical prote	S70876	2	294
604	5.6	66.5	ABC transporter, p	F81712	2	316
605	5.6	66.5	hypothetical prote	S77103	2	333
606	5.6	66.5	hypothetical prote	AD2201	2	347
607	5.6	66.5	hypothetical prote	T20737	2	356
608	5.6	66.5	conserved hypothet	P90055	2	359
609	5.6	66.5	hypothetical prote	S75836	2	367
610	5.6	66.5	hypothetical prote	G89786	2	380
611	5.6	66.5	dual specificity p	I38890	2	384
612	5.6	66.5	F16N3.13 [imported	E96516	2	389
613	5.6	66.5	D3 dopamine recept	G00013	2	400
614	5.6	66.5	hypothetical prote	G89773	2	412
615	5.6	66.5	polysaccharide tra	H95041	2	413
616	5.6	66.5	hypothetical prote	D98111	2	435
617	5.6	66.5	maltodextrin ABC t	G95246	2	435
618	5.6	66.5	MATE efflux family	B95135	2	453
619	5.6	66.5	cytochrome-c oxida	H71228	2	462
620	5.6	66.5	low-affinity inorg	G71969	2	488
621	5.6	66.5	cAMP receptor subt	D84998	2	490
622	5.6	66.5	efflux transporter	A46391	2	490
623	5.6	66.5	hypothetical prote	AC1555	2	491
624	5.6	66.5	hypothetical prote	A71875	2	493
625	5.6	66.5	hypothetical prote	T32644	2	494
626	5.6	66.5	nickel transport s	T27627	2	507
627	5.6	66.5	probable alkaline	G83720	2	539
628	5.6	66.5	probable alkaline	E91135	2	547
629	5.6	66.5	sterol O-acyltrans	H85980	2	547
630	5.6	66.5	sterol O-acyltrans	A48026	1	550
631	5.6	66.5	C-terminal domain	C71424	2	582
632	5.6	66.5	hypothetical prote	AI1510	2	583
633	5.6	66.5	cytochrome c-type	T32430	2	598
634	5.6	66.5	cytochrome c-type	AG2696	2	663
635	5.6	66.5	cytochrome c-type	G97478	2	663
636	5.6	66.5	Na+/Cl(-)-dependen	I56506	2	727
637	5.6	66.5	neurotransmitter t	S27043	2	727
638	5.6	66.5	genome polyprotein	S19876	2	782
639	5.6	66.5	hypothetical prote	B36786	2	862
640	5.6	66.5	hypothetical prote	T47311	2	889
641	5.6	66.5	hypothetical prote	T27479	2	992
642	5.6	66.5	Na+/Ca2+,K+-exchan	T31433	2	1014
643	5.6	66.5	protein F11A10.3 [	C88854	2	1083
644	5.6	66.5	DNA polymerase III	H81037	2	1144
645	5.6	66.5	hypothetical prote	T15961	2	1456
646	5.6	66.5	gravin - human	JW0057	2	1684
647	5.6	66.5	hypothetical prote	B85062	2	1768
648	5.6	66.5	genome polyprotein	S16449	1	2151
649	5.6	66.5	DNA-directed DNA p	G02434	2	2285
650	5.6	66.5	inositol 1,4,5-tri	A43360	2	2833
651	5.6	66.5	genome polyprotein	GNWVC3	1	3011
652	5.6	66	NADH2 dehydrogenas	S28759	2	93
653	5.5	66	diacylglycerol kin	D83820	2	130
654	5.5	66	conserved hypothet	A89801	2	209
655	5.5	66	hypothetical prote	H96816	2	276
656	5.5	66	hypothetical prote	S42125	2	279
657	5.5	66	sulfate ABC transp	D87447	2	285
658	5.5	66	sterol O-acyltrans	A99074	2	302
659	5.5	66	iron transport pro	I47040	2	305
660	5.5	66	hypothetical prote	B41671	1	317
661	5.5	66	hypothetical prote	B84291	2	318
662	5.5	66	hypothetical prote	E71137	2	322
663	5.5	66	conserved membrane	C97272	2	332
664	5.5	66	G protein-coupled	I52315	2	370
665	5.5	66	ubiquinol-cytochro	S17315	1	379
666	5.5	66	ubiquinol-cytochro	S17409	1	379
667	5.5	66	ubiquinol-cytochro	S58460	2	379
668	5.5	66	G protein-coupled	A35300	2	381
669	5.5	66	protein UL33 - hum	QOBET9	1	390
670	5.5	66	hypothetical prote	T21154	2	397
671	5.5	66	hypothetical prote	T44477	2	397
672	5.5	66	hypothetical prote	B70505	2	397
673	5.5	66	probable emulsan r	T44831	2	401
674	5.5	66	probable sugar tra	B64927	1	404
675	5.5	66	probable transport	A85777	2	404
676	5.5	66	probable transport	E90928	2	404
677	5.5	66	CBS domain protein	H86539	2	411
678	5.5	66	GGDEF family prote	A82444	2	412
679	5.5	66	hypothetical wtf5	T41027	2	418
680	5.5	66	hypothetical prote	B72353	2	418
681	5.5	66	probable phosphati	T07366	2	424
682	5.5	66	hypothetical prote	T14816	2	436
683	5.5	66	hypothetical prote	T18633	2	447
684	5.5	66	alpha-2B-adrenergi	A37223	2	450
685	5.5	66	alpha-2-adrenergic	A38316	2	450
686	5.5	66	ABC transporter pe	F86846	2	453

No.	Score	pI	Acc	N	Len	Description
687	66	5.5	S75369	2	483	hypothetical prote
688	66	5.5	T24238	2	484	hypothetical prote
689	66	5.5	B82940	2	496	hypothetical prote
690	66	5.5	G47677	2	508	glycerophosphoryl
691	66	5.5	T28306	2	525	ORF MSV145 hypothe
692	66	5.5	G69635	2	527	PTS arbutin-like e
693	66	5.5	A90037	2	532	hypothetical prote
694	66	5.5	A69890	2	546	hypothetical prote
695	66	5.5	B87423	2	548	cytochrome-c oxida
696	66	5.5	S45886	2	552	hypothetical prote
697	66	5.5	S73707	2	565	Na(+) translocatin
698	66	5.5	S07744	2	570	NADH2 dehydrogenas
699	66	5.5	S33212	1	573	INDA1 protein - fu
700	66	5.5	AF1418	2	573	ABC transporter, A
701	66	5.5	AH1793	2	619	ABC transporter, A
702	66	5.5	T11314	2	632	NADH2 dehydrogenas
703	66	5.5	T24405	2	654	hypothetical prote
704	66	5.5	A98350	2	654	hypothetical ABC t
705	66	5.5	AF2932	2	705	hypothetical prote
706	66	5.5	T48464	2	721	hypothetical prote
707	66	5.5	A70764	2	736	probable glgX prot
708	66	5.5	G01522	2	784	acidic 82 kDa prot
709	66	5.5	B90442	2	1039	tricorn proteinase
710	66	5.5	S76747	2	1054	hypothetical prote
711	66	5.5	A61221	2	1359	probable calcium t
712	66	5.5	T34036	2	1375	hypothetical prote
713	66	5.5	S48375	2	2599	hypothetical prote
714	66	5.5	P90608	2	2599	ABC transporter pe
715	66	5.5	I38344	1	26926	titin, cardiac mus
716	65.5	5.5	E97760	2	132	NADH2 dehydrogenas
717	65.5	5.5	B70074	2	132	hypothetical prote
718	65.5	5.5	G69447	2	146	hypothetical prote
719	65.5	5.5	AI3476	2	171	signal peptidase I
720	65.5	5.5	T17106	2	197	hypothetical prote
721	65.5	5.5	S67771	2	210	endoplasmic reticu
722	65.5	5.5	T43100	2	252	hypothetical prote
723	65.5	5.5	F69456	2	290	signal sequence pe
724	65.5	5.5	F86839	2	297	phosphate ABC tran
725	65.5	5.5	B83792	2	297	hypothetical prote
726	65.5	5.5	T21308	2	301	hypothetical prote
727	65.5	5.5	S23459	2	317	polysulfide reduct
728	65.5	5.5	T36087	2	327	probable binding p
729	65.5	5.5	S36003	1	348	NADH2 dehydrogenas
730	65.5	5.5	F82880	2	351	hypothetical ferri
731	65.5	5.5	F69629	2	365	spore germination
732	65.5	5.5	JC2056	2	367	prostaglandin E2 r
733	65.5	5.5	S58456	2	379	ubiquinol-cytochro
734	65.5	5.5	T32778	2	379	hypothetical prote
735	65.5	5.5	T32601	2	391	hypothetical prote
736	65.5	5.5	AH0362	2	394	nucleoside permeas
737	65.5	5.5	T11064	2	410	NADH2 dehydrogenas
738	65.5	5.5	B90569	2	423	conserved hypothet
739	65.5	5.5	A97688	2	425	hypothetical 45.5K
740	65.5	5.5	AF2913	2	425	conserved hypothet
741	65.5	5.5	T32832	2	429	hypothetical hypot
742	65.5	5.5	A42670	2	442	microfibril-associ
743	65.5	5.5	T38916	2	445	probable transcrip
744	65.5	5.5	H83629	2	449	probable dicarboxy
745	65.5	5.5	A75327	2	457	hypothetical prote
746	65.5	5.5	B75170	2	477	endoplasmic reticu
747	65.5	5.5	A97022	2	480	type I site-specif
748	65.5	5.5	A97928	2	487	cytochrome-c oxida
749	65.5	5.5	H64537	1	488	cytochrome-c oxida
750	65.5	5.5	G81295	2	488	efflux transporter
751	65.5	5.5	AE1197	2	491	probably membrane
752	65.5	5.5	A97022	2	495	hypothetical prote
753	65.5	5.5	G84706	2	500	NADH2 dehydrogenas
754	65.5	5.5	AD3395	2	502	hypothetical prote
755	65.5	5.5	T25669	2	502	probable folate tr
756	65.5	5.5	A53207	2	518	delayed rectifier
757	65.5	5.5	T34417	2	528	probable ABC trans
758	65.5	5.5	B84825	2	544	hypothetical prote
759	65.5	5.5	E90460	2	545	hypothetical prote

No.	Acc	N	Len	pI	Score	Description
760	S71189	2	561	5.5	65.5	Dwarf1 protein - A
761	AH1417	2	575	5.5	65.5	ABC transporter (A
762	T15736	2	578	5.5	65.5	hypothetical prote
763	AH1151	2	583	5.5	65.5	glycerophosphoryl
764	C81316	2	590	5.5	65.5	probable sugar epi
765	B82881	2	597	5.5	65.5	hypothetical prote
766	AB1167	2	617	5.5	65.5	phosphotransferase
767	AC1204	2	618	5.5	65.5	phosphotransferase
768	H70331	2	642	5.5	65.5	ATP-dependent heli
769	A56851	2	718	5.5	65.5	Na+/myo-inositol c
770	H82198	2	720	5.5	65.5	RTX toxin transpor
771	AF1254	2	721	5.5	65.5	penicillin-binding
772	S61568	2	740	5.5	65.5	probable membrane
773	QRHULD	1	860	5.5	65.5	LDL receptor precu
774	AC0204	2	958	5.5	65.5	probable integral
775	S41797	1	1087	5.5	65.5	cellulose 1,4-beta
776	B22999	1	1328	5.5	65.5	TyB protein - yea
777	S74293	2	1427	5.5	65.5	SRB8 protein - yea
778	B71636	2	1581	5.5	65.5	hypothetical prote
779	T32452	2	1635	5.5	65.5	hypothetical prote
780	AD0340	1	126	5.4	65	probable membrane
781	C69393	2	149	5.4	65	transcription regu
782	Q1AD25	1	176	5.4	65	early E1B 21K prot
783	S40728	1	196	5.4	65	hypothetical prote
784	MMIHIV	2	225	5.4	65	E1 membrane glycop
785	I48149	2	247	5.4	65	serotonin receptor
786	B75099	2	259	5.4	65	hypothetical prote
787	A47112	2	271	5.4	65	growth response pr
788	B89950	2	280	5.4	65	hemA concentration
789	S75957	2	290	5.4	65	nitrate transport
790	T02877	2	291	5.4	65	probable chlorophy
791	C97453	2	291	5.4	65	cytochrome c oxida
792	AE2671	2	307	5.4	65	cytochrome c oxida
793	B36125	2	313	5.4	65	branched-chain ami
794	A64084	2	319	5.4	65	lysophospholipase
795	D87087	2	322	5.4	65	hypothetical prote
796	S38091	2	330	5.4	65	hypothetical prote
797	H75068	2	338	5.4	65	dipeptide abc tran
798	H75029	2	344	5.4	65	hypothetical prote
799	S50339	2	345	5.4	65	NADH2 dehydrogenas
800	AD1200	2	355	5.4	65	conserved hypothet
801	T12361	2	359	5.4	65	NADH2 dehydrogenas
802	G70200	2	362	5.4	65	hypothetical prote
803	T15249	2	375	5.4	65	hypothetical prote
804	H69785	2	379	5.4	65	mannan endo-1,4-be
805	I38879	2	379	5.4	65	corticotropin rele
806	S17414	1	379	5.4	65	ubiquinol-cytochro
807	S58461	2	380	5.4	65	ubiquinol-cytochro
808	S58455	2	382	5.4	65	ubiquinol-cytochro
809	D34285	2	390	5.4	65	ubiquinol-cytochro
810	T11138	2	415	5.4	65	hypothetical prote
811	C84984	1	438	5.4	65	conserved hypothet
812	T21532	2	442	5.4	65	hypothetical prote
813	B81410	2	445	5.4	65	probable integral
814	A83122	2	457	5.4	65	probable MFS trans
815	AD2358	2	462	5.4	65	glucosyltransferas
816	T28334	2	477	5.4	65	Ser/Thr protein ki
817	B88613	2	479	5.4	65	protein T27E9.5 [i
818	S54508	2	481	5.4	65	probable membrane
819	A69036	2	490	5.4	65	TRK system potassi
820	B81050	2	492	5.4	65	cytochrome-c oxida
821	T14545	2	510	5.4	65	probable sugar tra
822	S59107	2	511	5.4	65	NADH2 dehydrogenas
823	S55204	2	513	5.4	65	hypothetical prote
824	H75097	2	526	5.4	65	polysaccharide bio
825	T37180	2	530	5.4	65	probable membrane
826	D91047	2	535	5.4	65	hydrogenase 4 memb
827	B89771	2	539	5.4	65	hypothetical prote
828	A64697	2	547	5.4	65	conserved hypothet
829	S55190	2	547	5.4	65	hypothetical prote
830	T31543	2	576	5.4	65	hypothetical prote
831	S53920	2	547	5.4	65	SNG1 protein - yea
832	T25375	2	576	5.4	65	hypothetical prote

Seq	Accession	Count	Length	Score	Value	Description
833	S61131	2	579	5.4	65	probable membrane
834	S65298	2	608	5.4	65	dicarboxylic amino
835	T21747	2	611	5.4	65	hypothetical amino
836	G82508	2	624	5.4	65	hypothetical prote
837	T11125	2	627	5.4	65	NADH2 dehydrogenas
838	P84483	2	633	5.4	65	Mutator-like trans
839	D69957	2	638	5.4	65	conserved hypothet
840	F97787	2	643	5.4	65	sodium/pantothenat
841	A45515	2	676	5.4	65	dnaK-type molecula
842	P86394	2	684	5.4	65	protein T24P13.20
843	H84791	2	697	5.4	65	hypothetical prote
844	T13505	2	702	5.4	65	NADH2 dehydrogenas
845	T04400	2	705	5.4	65	NADH2 dehydrogenas
846	H96818	2	773	5.4	65	hypothetical prote
847	G83816	2	773	5.4	65	late competence op
848	T04459	2	808	5.4	65	hypothetical prote
849	S77086	2	861	5.4	65	hypothetical prote
850	T38518	2	927	5.4	65	ribonuclease II RN
851	F84637	2	931	5.4	65	probable plasma me
852	T01809	2	938	5.4	65	hypothetical prote
853	C70522	2	1089	5.4	65	probable mmpL8 pro
854	D64315	2	1163	5.4	65	type I restriction
855	S76370	2	1178	5.4	65	sensory transducti
856	I38496	2	1232	5.4	65	anion exchanger 3
857	T34225	2	1421	5.4	65	hypothetical prote
858	T17464	2	5069	5.4	65	rifamycin polyketi
859	T41339	2	180	5.4	64.5	hypothetical prote
860	S35280	2	211	5.4	64.5	eaC protein - phag
861	AE0395	2	217	5.4	64.5	probable amino aci
862	C69432	2	227	5.4	64.5	hypothetical prote
863	E96957	2	234	5.4	64.5	HAD superfamily hy
864	AF2470	2	268	5.4	64.5	potassium channel
865	E81384	2	271	5.4	64.5	prolipoprotein dia
866	T43119	2	275	5.4	64.5	hypothetical prote
867	D71517	2	293	5.4	64.5	probable metal tra
868	T32202	2	295	5.4	64.5	hypothetical prote
869	T27584	2	297	5.4	64.5	hypothetical prote
870	T23904	2	320	5.4	64.5	protein F13E6.6 [i
871	A86411	2	326	5.4	64.5	hypothetical prote
872	F64175	2	353	5.4	64.5	hypothetical prote
873	T22823	2	358	5.4	64.5	hypothetical prote
874	A86841	2	361	5.4	64.5	hypothetical prote
875	A40734	2	361	5.4	64.5	Pas (Passover) pro
876	S43264	2	379	5.4	64.5	ubiquinol-cytochro
877	T11505	1	379	5.4	64.5	ubiquinol-cytochro
878	S58454	2	379	5.4	64.5	ubiquinol-cytochro
879	A53077	2	379	5.4	64.5	ubiquinol-cytochro
880	CBMS	1	381	5.4	64.5	pituitary adenylat
881	S33449	2	381	5.4	64.5	hypothetical prote
882	H69154	2	385	5.4	64.5	phosphoglycerate k
883	H95057	2	398	5.4	64.5	phosphoglycerate k
884	A97927	2	398	5.4	64.5	d3 dopamine recept
885	G01977	2	400	5.4	64.5	LAG1 protein - yea
886	S46800	2	411	5.4	64.5	rod shape-determin
887	AF1127	2	416	5.4	64.5	UDP-N-acetylglucos
888	T45800	2	426	5.4	64.5	NADH2 dehydrogenas
889	T11162	2	433	5.4	64.5	probable maltodext
890	AC0105	2	435	5.4	64.5	NADH2 dehydrogenas
891	C22845	2	439	5.4	64.5	hypothetical prote
892	A84153	2	439	5.4	64.5	hypothetical prote
893	B26696	2	443	5.4	64.5	NADH2 dehydrogenas
894	T11474	2	444	5.4	64.5	P44 hepatitis-asso
895	A43676	2	444	5.4	64.5	microtubular aggre
896	S48218	2	444	5.4	64.5	dopamine receptor
897	DYRTD3	1	446	5.4	64.5	hypothetical prote
898	D85362	2	448	5.4	64.5	probable histidine
899	S57909	2	448	5.4	64.5	hypothetical prote
900	T23528	2	450	5.4	64.5	two-component sens
901	D70045	2	451	5.4	64.5	pituitary adenylat
902	JN0616	2	467	5.4	64.5	transpoase C - Ba
903	C29051	2	478	5.4	64.5	glycinin chain Ala
904	FWSYG2	1	495	5.4	64.5	glycinin G1 precur
905	S10851	2	495	5.4	64.5	glycinin G1 precur

Seq	Accession	Count	Length	Score	Value	Description
906	S39061	2	495	5.4	64.5	pituitary adenylyl
907	S36114	2	495	5.4	64.5	pituitary adenylat
908	H64964	2	512	5.4	64.5	probable membrane
909	A99549	2	521	5.4	64.5	amino acid permeas
910	S39060	2	523	5.4	64.5	pituitary adenylyl
911	H65107	2	547	5.4	64.5	hypothetical 61.6
912	A56730	2	554	5.4	64.5	carl protein - Pod
913	B97812	2	555	5.4	64.5	virulence factor m
914	AB1793	2	575	5.4	64.5	ABC transporter (A
915	T05904	2	576	5.4	64.5	cytochrome P450 97
916	B89869	2	614	5.4	64.5	hypothetical prote
917	AC1236	2	622	5.4	64.5	acyltransferase (t
918	QQBY2M	1	638	5.4	64.5	mRNA maturase bI4
919	T26307	2	715	5.4	64.5	hypothetical prote
920	T47648	2	720	5.4	64.5	ABC transporter-li
921	AD1617	2	721	5.4	64.5	penicillin-binding
922	AB1491	2	721	5.4	64.5	hypothetical prote
923	AD0341	2	735	5.4	64.5	hypothetical prote
924	AD1070	2	763	5.4	64.5	probable membrane
925	A89862	2	801	5.4	64.5	phosphatidylglycer
926	H64568	2	803	5.4	64.5	Na+/H+ antiporter
927	T30715	2	889	5.4	64.5	probable major cor
928	A70848	2	979	5.4	64.5	probable membrane
929	JC8066	2	1007	5.4	64.5	138K protein - Tet
930	JH0284	2	1114	5.4	64.5	125K surface antig
931	B70723	2	1146	5.4	64.5	probable mmpL12 pr
932	T48829	2	1154	5.4	64.5	related to SREBP c
933	S45628	2	1465	5.4	64.5	DNA-directed DNA p
934	S69688	2	1529	5.4	64.5	hypothetical prote
935	S64403	2	1630	5.4	64.5	ESP1 protein - yea
936	S64800	2	1661	5.4	64.5	probable membrane
937	GNWVJ8	1	3033	5.4	64.5	genome polyprotein
938	A70041	2	202	5.4	64	conserved hypothet
939	G82359	2	209	5.4	64	conserved hypothet
940	JC5347	2	253	5.4	64	cdd3 protein - Clo
941	T12451	2	259	5.4	64	hypothetical prote
942	H69768	2	269	5.4	64	conserved hypothet
943	P89632	2	270	5.4	64	protein F13E6.3 [i
944	T50567	2	274	5.4	64	protein F3M18.6 [i
945	C70040	2	276	5.4	64	plant-metabolite d
946	S48358	2	276	5.4	64	probable membrane
947	C95932	2	281	5.4	64	probable sugar upt
948	D83009	2	283	5.4	64	probable permease
949	B83883	2	285	5.4	64	sugar transport sy
950	S36955	2	288	5.4	64	cytochrome-c oxida
951	T29675	2	330	5.4	64	hypothetical prote
952	A48258	2	342	5.4	64	dopamine receptor
953	T11248	2	347	5.4	64	NADH2 dehydrogenas
954	S56716	2	351	5.4	64	protein kinase SPK
955	G01430	1	351	5.4	64	PL6 protein - huma
956	T20271	2	367	5.4	64	hypothetical prote
957	H90587	2	369	5.4	64	hypothetical prote
958	S26031	1	370	5.4	64	ubiquinol-cytochro
959	G82656	2	376	5.4	64	ubiquinol-cytochro
960	D64181	2	378	5.4	64	twitching motility
961	CBBO	2	379	5.4	64	probable cytochrom
962	S17419	1	379	5.4	64	ubiquinol-cytochro
963	S26163	1	379	5.4	64	ubiquinol-cytochro
964	S43263	1	379	5.4	64	ubiquinol-cytochro
965	T11414	2	379	5.4	64	ubiquinol-cytochro
966	S58452	2	379	5.4	64	ubiquinol-cytochro
967	S58459	2	379	5.4	64	ubiquinol-cytochro
968	S55594	2	383	5.4	64	G protein-coupled
969	G64667	2	383	5.4	64	NA+/H+ antiporter
970	H71848	2	383	5.4	64	probable na+/h+ an
971	S74522	2	387	5.4	64	hypothetical prote
972	AD1417	2	402	5.4	64	drug-efflux transp
973	A97559	2	404	5.4	64	hypothetical prote
974	AE2779	2	404	5.4	64	acyltransferase [i
975	S26021	2	409	5.4	64	NADH2 dehydrogenas
976	A55610	2	411	5.4	64	corticotropin-rele
977	H81659	2	413	5.4	64	branched-chain ami
978	E84338	2	422	5.4	64	isocitrate dehydro

Seq			Acc			Description
979	5.4	64	S32570	430	1	malC protein – Str
980	5.4	64	B40392	450	2	alpha-2-adrenergic
981	5.4	64	A36908	451	2	spore cortex penic
982	5.4	64	T31258	455	2	aromatic oxygenase
983	5.4	64	AF2975	457	2	aminotransferase,
984	5.4	64	E98307	457	2	probable aminotran
985	5.4	64	AC0281	463	2	probable amino aci
986	5.4	64	H90322	469	2	polysaccharide bio
987	5.4	64	E58931	492	2	NADH2 dehydrogenas
988	5.4	64	JC7627	503	2	cytochrome P450 3A
989	5.4	64	T40334	511	2	hypothetical prote
990	5.4	64	A75122	527	2	sodium- and chlori
991	5.4	64	T36109	536	2	hypothetical prote
992	5.4	64	C90406	538	2	conserved hypothet
993	5.4	64	T13877	544	2	NADH2 dehydrogenas
994	5.4	64	T52481	562	2	cytochrome-c oxida
995	5.4	64	G75282	575	2	probable glutathio
996	5.4	64	A34400	586	1	ezrin [validated]
997	5.4	64	T05130	598	2	hypothetical prote
998	5.4	64	C75120	602	2	hypothetical prote
999	5.4	64	B69805	606	2	conserved hypothet
1000	5.4	64	G02640	608	2	polycystic kidney
1001	5.4	64	F70512	609	2	probable ATPase -
1002	5.4	64	S37049	610	2	H+-exporting ATPas
1003	5.4	64	A69845	614	2	Na+/H+ antiporter
1004	5.4	64	T47177	630	2	hypothetical prote
1005	5.4	64	C86677	654	2	DNA ligase (NAD) (
1006	5.4	64	T52460	657	2	hypothetical prote
1007	5.4	64	T51779	661	2	non-phototropic hy
1008	5.4	64	T50347	674	2	hypothetical prote
1009	5.4	64	AB1566	696	2	hypothetical prote
1010	5.4	64	T10651	748	2	hypothetical prote
1011	5.4	64	A87754	802	2	protein C43E1.11
1012	5.4	64	H82939	838	2	conserved hypothet
1013	5.4	64	T37768	860	2	probable vacuolar
1014	5.4	64	B86322	874	2	F6A14.8 protein -
1015	5.4	64	AF1409	896	2	the two components
1016	5.4	64	S57385	991	2	probable membrane
1017	5.4	64	RNZQBF	1024	1	DNA-directed RNA p
1018	5.4	64	T19745	1078	2	hypothetical prote
1019	5.4	64	B81303	1081	2	probable membrane
1020	5.4	64	A33638	1227	2	erythrocyte anion
1021	5.4	64	T13415	1385	2	hypothetical prote
1022	5.4	64	DJHUAC	1462	1	DNA-directed DNA p
1023	5.4	64	JE0084	1695	2	voltage-gated sodi
1024	5.4	64	A71616	2496	2	secreted protein P
1025	5.3	63.5	S43115	111	2	acidic ribosqmal p
1026	5.3	63.5	G71692	123	2	NADH2 dehydrogenas
1027	5.3	63.5	AH0495	147	2	probable membrane
1028	5.3	63.5	H70581	149	2	hypothetical prote
1029	5.3	63.5	B71000	195	2	conserved hypothet
1030	5.3	63.5	C90191	214	2	hypothetical prote
1031	5.3	63.5	B71925	218	2	cag island protein
1032	5.3	63.5	T29205	218	2	hypothetical prote
1033	5.3	63.5	F85679	231	2	probable antiepre
1034	5.3	63.5	S75336	238	2	hypothetical prote
1035	5.3	63.5	P86691	241	2	ABC transporter pe
1036	5.3	63.5	S74794	242	1	hypothetical prote
1037	5.3	63.5	AD3574	246	2	branchedD-chain ami
1038	5.3	63.5	AF0106	259	2	probable membrane
1039	5.3	63.5	E95161	275	2	hypothetical prote
1040	5.3	63.5	D98027	275	2	hypothetical prote
1041	5.3	63.5	G84320	275	2	conserved membrane
1042	5.3	63.5	B96951	276	2	hypothetical prote
1043	5.3	63.5	T16240	280	2	hypothetical prote
1044	5.3	63.5	AB0346	282	2	probable ABC trans
1045	5.3	63.5	B83086	282	2	conserved hypothet
1046	5.3	63.5	AB2939	291	2	hypothetical prote
1047	5.3	63.5	E98343	291	2	hypothetical prote
1048	5.3	63.5	F75571	291	2	hypothetical prote
1049	5.3	63.5	D26696	313	2	NADH2 dehydrogenas
1050	5.3	63.5	B69365	315	2	hypothetical prote
1051	5.3	63.5	H86665	316	2	ferrichrome ABC tr

Description	Acc					Seq
MDCR15 protein - h	S56162	2	327	5.3	63.5	1052
oligopeptide ABC t	D98215	2	328	5.3	63.5	1053
septin homolog - f	T39824	2	328	5.3	63.5	1054
oligopeptide ABC t	B72393	2	334	5.3	63.5	1055
hypothetical prote	T41037	2	334	5.3	63.5	1056
hypothetical prote	T27081	2	342	5.3	63.5	1057
spa40 protein - Sh	A38908	2	342	5.3	63.5	1058
probable integral	T34981	2	344	5.3	63.5	1059
hypothetical prote	T15203	2	355	5.3	63.5	1060
hypothetical prote	D90172	2	359	5.3	63.5	1061
hypothetical prote	AE3071	2	361	5.3	63.5	1062
oligopeptide trans	AB3494	2	365	5.3	63.5	1063
G protein-coupled	S26667	2	372	5.3	63.5	1064
probable aspartate	B72275	2	377	5.3	63.5	1065
ubiquinol-cytochro	CBRT	2	380	5.3	63.5	1066
ubiquinol-cytochro	T11312	2	381	5.3	63.5	1067
protein K10B4.2 [i	H88012	2	387	5.3	63.5	1068
hypothetical prote	G75133	2	389	5.3	63.5	1069
probable hth trans	H71520	2	392	5.3	63.5	1070
transmembrane tran	B81358	2	395	5.3	63.5	1071
ubiquinol-cytochro	C71682	2	398	5.3	63.5	1072
probable periplasm	D81397	2	398	5.3	63.5	1073
cell division prot	B95080	2	399	5.3	63.5	1074
phosphoglycerate k	AG3016	2	400	5.3	63.5	1075
hypothetical prote	T46306	2	401	5.3	63.5	1076
latent membrane pr	LABECA	1	404	5.3	63.5	1077
hypothetical prote	T19887	2	406	5.3	63.5	1078
CDP-diacylglycerol	T04915	2	423	5.3	63.5	1079
CDP-diacylglycerol	G85255	2	423	5.3	63.5	1080
phosphoglycerate k	A96268	2	426	5.3	63.5	1081
hypothetical prote	T33299	2	426	5.3	63.5	1082
conserved hypothet	A82262	2	438	5.3	63.5	1083
hypothetical prote	B85789	2	444	5.3	63.5	1084
hypothetical prote	T16025	2	445	5.3	63.5	1085
hypothetical prote	F90940	2	447	5.3	63.5	1086
CDP-diacylglycerol	S52437	2	447	5.3	63.5	1087
hypothetical prote	B96738	2	450	5.3	63.5	1088
hypothetical prote	T21118	2	452	5.3	63.5	1089
sugar transferase	C97187	2	461	5.3	63.5	1090
hypothetical prote	T48686	2	468	5.3	63.5	1091
mg2+ transport pro	H90562	2	485	5.3	63.5	1092
hypothetical prote	B95059	2	487	5.3	63.5	1093
hypothetical prote	A64939	2	491	5.3	63.5	1094
sugar transport re	B90373	2	492	5.3	63.5	1095
integral membrane	S76516	2	494	5.3	63.5	1096
transporter like p	T48385	2	498	5.3	63.5	1097
hypothetical prote	T16190	2	498	5.3	63.5	1098
NADH dehydrogenase	AF2325	2	500	5.3	63.5	1099
hypothetical prote	G90321	2	511	5.3	63.5	1100
virulence factor m	A70201	2	512	5.3	63.5	1101
nucleocapsid prote	A49601	2	525	5.3	63.5	1102
conserved hypothet	G82873	2	537	5.3	63.5	1103
sterol O-acyltrans	I49454	2	540	5.3	63.5	1104
uncharacterized me	C96943	2	544	5.3	63.5	1105
L-lactate permease	B64537	2	551	5.3	63.5	1106
l-lactate permease	D71969	2	551	5.3	63.5	1107
probable peptide t	G96744	2	555	5.3	63.5	1108
probable L-lactate	C75340	2	567	5.3	63.5	1109
hyaluronoglucosami	T17588	2	568	5.3	63.5	1110
sodium/dicarboxyla	I46528	2	593	5.3	63.5	1111
protein ZK697.5 [i	E88956	2	594	5.3	63.5	1112
glucose transport	A36361	2	605	5.3	63.5	1113
probable flagellar	H71562	2	605	5.3	63.5	1114
hypothetical proce	T43974	2	605	5.3	63.5	1115
hypothetical prote	T44161	2	610	5.3	63.5	1116
ba-type ubiquinol	B54759	2	668	5.3	63.5	1117
protein kinase C (	B37237	2	671	5.3	63.5	1118
probable type III	AF0697	2	681	5.3	63.5	1119
hypothetical prote	A85044	2	683	5.3	63.5	1120
killer toxin KHS p	JQ1148	2	708	5.3	63.5	1121
hypothetical prote	T20314	2	741	5.3	63.5	1122
probable transport	T48189	2	780	5.3	63.5	1123
cell division prot	A70132	2	787	5.3	63.5	1124

No.			Num	Ct	Accession	Description
1125	63.5	5.3	819	2	T19351	hypothetical prote
1126	63.5	5.3	841	2	T38703	hypothetical prote
1127	63.5	5.3	843	2	T32482	hypothetical prote
1128	63.5	5.3	844	2	T41237	conserved hypothet
1129	63.5	5.3	951	2	AD2339	hypothetical prote
1130	63.5	5.3	966	2	T08987	probable cadmium-t
1131	63.5	5.3	1004	2	H97717	hypothetical prote
1132	63.5	5.3	1098	2	G87323	hypothetical prote
1133	63.5	5.3	1229	2	S38100	hypothetical prote
1134	63.5	5.3	1351	2	S42391	SIP3 protein - yea
1135	63.5	5.3	1388	2	C71607	hypothetical prote
1136	63.5	5.3	1407	2	T17269	hypothetical prote
1137	63.5	5.3	1408	1	T00558	probable ABC trans
1138	63.5	5.3	1545	2	T47671	P-glycoprotein-lik
1139	63.5	5.3	1545	2	T42751	sulfonylurea recep
1140	63.5	5.3	1769	2	T46645	sulfonylurea recep
1141	63.5	5.3	2357	2	S53378	probable membrane
1142	63.5	5.3	4725	1	A59249	class VII unconven
1143	63.5	5.3	4725	1	A44357	dynein heavy chain
1144	63	5.3	96	1	WMVZP3	F3 protein - fowlp
1145	63	5.3	103	2	T20878	hypothetical prote
1146	63	5.3	175	2	D70945	hypothetical prote
1147	63	5.3	230	2	B81705	conserved hypothet
1148	63	5.3	230	2	T17506	hypothetical prote
1149	63	5.3	236	2	F83520	phosphoribosylamin
1150	63	5.3	249	2	T01891	hypothetical prote
1151	63	5.3	257	2	S01165	achaete-scute locu
1152	63	5.3	258	2	H65188	sec-independent pr
1153	63	5.3	258	2	P86071	sec-independent pr
1154	63	5.3	258	2	H91224	Sec-independent pr
1155	63	5.3	280	2	D84015	maltose/maltodextr
1156	63	5.3	288	2	S36954	cytochrome-c oxida
1157	63	5.3	290	2	S48301	geranylgeranyl tra
1158	63	5.3	301	2	T50001	hypothetical;prote
1159	63	5.3	306	2	H83620	probable permease
1160	63	5.3	313	2	A86743	hypothetical prote
1161	63	5.3	322	2	B90013	hypothetical,prote
1162	63	5.3	329	2	B77790	protein B0207.4 [i
1163	63	5.3	332	2	B84943	conserved hypothet
1164	63	5.3	339	2	D89880	conserved hypothet
1165	63	5.3	345	2	T12364	NADH2 dehydrogenas
1166	63	5.3	358	2	B83808	hypothetical;prote
1167	63	5.3	359	2	S56720	probable serine/th
1168	63	5.3	361	2	A45211	prostaglandin E re
1169	63	5.3	362	2	T29552	hypothetical prote
1170	63	5.3	362	2	C69804	surface adhesion h
1171	63	5.3	364	2	S65009	prostaglandin E re
1172	63	5.3	365	2	A42414	prostaglandin E re
1173	63	5.3	378	1	S17411	ubiquinol-cytochro
1174	63	5.3	379	1	S41833	ubiquinol-cytochro
1175	63	5.3	379	1	S41847	ubiquinol-cytochro
1176	63	5.3	379	1	S43265	ubiquinol-cytochro
1177	63	5.3	379	1	T11492	ubiquinol-cytochro
1178	63	5.3	379	2	S58085	ubiquinol-cytochro
1179	63	5.3	382	2	S58464	NADH2 dehydrogenas
1180	63	5.3	386	2	S47882	aromatic amino aci
1181	63	5.3	386	2	S60646	aspartate transami
1182	63	5.3	389	2	H95003	molybdopterin bios
1183	63	5.3	389	2	C97876	cell division prot
1184	63	5.3	391	2	D64541	proton/sodium-glut
1185	63	5.3	396	2	E97947	hypothetical prote
1186	63	5.3	398	2	B70415	arsenite transport
1187	63	5.3	405	2	T20902	corticotropin-rele
1188	63	5.3	411	2	G90154	cyclin Ia - maize
1189	63	5.3	415	2	S39535	hypothetical prote
1190	63	5.3	420	2	A57742	hypothetical prote
1191	63	5.3	431	2	T23809	hypothetical prote
1192	63	5.3	448	2	T30982	alpha-2A-adrenergi
1193	63	5.3	450	2	A34169	hypothetical prote
1194	63	5.3	469	2	AE2188	hypothetical prote
1195	63	5.3	475	2	S52893	hypothetical prote
1196	63	5.3	478	2	C59095	probable permease
1198	63	5.3	480	2	B70367	hypothetical prote
1199	63	5.3	481	2	S60260	stomatin-like prot
1200	63	5.3	490	2	C71541	probable na-depend
1201	63	5.3	491	2	AC1499	transmembrane prot
1202	63	5.3	493	2	T02376	hypothetical prote
1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1204	63	5.3	508	2	E90594	amino acid permeas
1205	63	5.3	509	1	A48528	membrane glycoprot
1206	63	5.3	527	2	T40744	probable nuclear d
1207	63	5.3	531	2	AH1491	hypothetical prote
1208	63	5.3	533	2	T06153	hypothetical prote
1209	63	5.3	534	2	A99316	hypothetical prote
1210	63	5.3	535	2	AF1835	probable ABC trans
1211	63	5.3	562	2	B70081	hypothetical prote
1212	63	5.3	565	2	B86359	protein similar to
1213	63	5.3	569	2	C70136	flagellar basal-bo
1214	63	5.3	574	2	T47566	hypothetical prote
1215	63	5.3	579	2	AB2177	hypothetical prote
1216	63	5.3	583	2	G84829	probable PTR2 fami
1217	63	5.3	584	2	G89789	two-component sens
1218	63	5.3	598	2	S66954	probable membrane
1219	63	5.3	600	2	B83875	two-component sens
1220	63	5.3	608	2	AD2000	ABC transporter AT
1221	63	5.3	677	2	T26574	hypothetical prote
1222	63	5.3	682	2	F95910	probable membrane-
1223	63	5.3	682	1	H64485	replication licens
1224	63	5.3	701	2	T13568	NADH2 dehydrogenas
1225	63	5.3	702	2	T12677	NADH2 dehydrogenas
1226	63	5.3	704	2	T13665	NADH2 dehydrogenas
1227	63	5.3	712	2	D87418	proton pump, proba
1228	63	5.3	729	2	T06127	probable sugar tra
1229	63	5.3	737	2	I39547	S-protein secretio
1230	63	5.3	738	2	S58612	NADH2 dehydrogenas
1231	63	5.3	769	2	G95270	hypothetical prote
1232	63	5.3	813	2	T02672	hypothetical prote
1233	63	5.3	849	2	C97740	protein H26D21.2 [
1234	63	5.3	869	2	S49844	probable membrane
1235	63	5.3	943	2	B45082	neurotrophic recep
1236	63	5.3	960	2	T17297	hypothetical prote
1237	63	5.3	1030	2	A42497	anion exchanger 3,
1238	63	5.3	1034	2	B86880	SWI/SNF family hel
1239	63	5.3	1082	2	H70360	cation efflux syst
1240	63	5.3	1212	2	B82809	exodeoxyribonuclea
1241	63	5.3	1227	2	B34911	band 3-related pro
1242	63	5.3	1532	2	T18438	hypothetical prote
1243	63	5.3	1646	2	JH0422	voltage-dependent
1244	63	5.3	1854	2	T39035	putative sodium ch
1245	63	5.3	2203	2	T42742	voltage-dependent
1246	63	5.3	2295	2	B71621	probable membrane
1247	62.5	5.3	4488	1	RRIHM2	genome polyprotein
1248	62.5	5.2	107	2	B69262	hypothetical prote
1249	62.5	5.2	140	2	B86739	potassium channel
1250	62.5	5.2	149	2	B83851	hypothetical prote
1251	62.5	5.2	168	2	JC1169	DNA-damage-inducib
1252	62.5	5.2	173	2	D71702	hypothetical prote
1253	62.5	5.2	178	2	S67379	hypothetical prote
1254	62.5	5.2	181	2	G82911	hypothetical prote
1255	62.5	5.2	200	2	A71895	hypothetical prote
1256	62.5	5.2	232	2	T22698	hypothetical prote
1257	62.5	5.2	236	2	F83705	hypothetical prote
1258	62.5	5.2	240	2	H70091	hypothetical prote
1259	62.5	5.2	244	2	T20810	hypothetical prote
1260	62.5	5.2	245	2	S10658	hypothetical prote
1261	62.5	5.2	258	2	E91201	type III secretion
1262	62.5	5.2	258	2	A86048	escT [imported] -
1263	62.5	5.2	274	2	AC2946	hypothetical prote
1264	62.5	5.2	274	2	G98336	sorbitol/mannitol
1265	62.5	5.2	276	2	G72292	glycerol-3-phospha
1266	62.5	5.2	276	2	H83568	probable permease
1267	62.5	5.2	280	2	T24579	probable permease
1268	62.5	5.2	283	2	T11063	NADH2 dehydrogenas
1269	62.5	5.2	289	2	D82504	phosphate ABC tran
1270	62.5	5.2	293	2	AH0075	probable permease

No			Code	Len		Description
1271	5.2	62.5	H83480	296	2	cytochrome o ubiqu
1272	5.2	62.5	T37251	298	2	homeobox protein c
1273	5.2	62.5	T26365	299	2	hypothetical prote
1274	5.2	62.5	C90272	326	2	hypothetical prote
1275	5.2	62.5	AB1925	333	2	protein R08F11.2 [
1276	5.2	62.5	B89010	333	2	hypothetical prote
1277	5.2	62.5	T41426	335	2	hypothetical wtf8
1278	5.2	62.5	H95060	349	2	ABC transporter, p
1279	5.2	62.5	D97929	349	2	hypothetical prote
1280	5.2	62.5	E81450	352	2	probable integral
1281	5.2	62.5	E83829	358	2	hypothetical prote
1282	5.2	62.5	F82210	365	2	amino acid ABC tra
1283	5.2	62.5	C88030	369	2	protein F46F5.10 [
1284	5.2	62.5	C69309	370	2	conserved hypothet
1285	5.2	62.5	S17407	379	1	ubiquinol-cytochro
1286	5.2	62.5	S58462	379	2	ubiquinol-cytochro
1287	5.2	62.5	S58057	379	2	ubiquinol-cytochro
1288	5.2	62.5	A72373	382	2	conserved hypothet
1289	5.2	62.5	A44227	383	1	omega-3 fatty acid
1290	5.2	62.5	F84771	383	2	hypothetical prote
1291	5.2	62.5	T31738	383	2	hypothetical prote
1292	5.2	62.5	C64722	388	2	Na+/H+-exchanging
1293	5.2	62.5	A86632	391	2	aromatic amino aci
1294	5.2	62.5	H84087		2	sodium/glutamate s
1295	5.2	62.5	H83249	399	2	BBRF3 protein - hu
1296	5.2	62.5	Q0BE35	404	1	protein T22F3.11 [
1297	5.2	62.5	H89006	405	2	conserved hypothet
1298	5.2	62.5	C89942	406	2	multidrug resistan
1299	5.2	62.5	AC1369	409	2	glucose 6 phosphat
1300	5.2	62.5	T51467	413	2	conserved hypothet
1301	5.2	62.5	D95018	417	2	conserved hypothet
1302	5.2	62.5	E97891	420	2	probable nanT prot
1303	5.2	62.5	C70518	420	2	flagellin [importe
1304	5.2	62.5	E97172	422	2	ct266 hypothetical
1305	5.2	62.5	A72080	425	2	CT266 hypothetical
1306	5.2	62.5	E86542	426	2	hypothetical prote
1307	5.2	62.5	H84069	426	2	hypothetical prote
1308	5.2	62.5	T20092	431	2	hypothetical prote
1309	5.2	62.5	JQ1042	440	2	endothelin recepto
1310	5.2	62.5	F30010	442	2	NADH2 dehydrogenas
1311	5.2	62.5	T08136	443	2	probable omega-6 d
1312	5.2	62.5	G85647	452	2	hypothetical prote
1313	5.2	62.5	G90787	452	2	hypothetical prote
1314	5.2	62.5	G64844	452	2	probable membrane
1315	5.2	62.5	D97217	455	2	glycosyltransferas
1316	5.2	62.5	F69662	457	2	UDP-N-acetylmuramo
1317	5.2	62.5	AF3284	459	2	high-affinity bran
1318	5.2	62.5	S57713	461	2	probable mannosyl
1319	5.2	62.5	A49131	468	2	inositol 1,4,5-tri
1320	5.2	62.5	C70641	470	1	hypothetical prote
1321	5.2	62.5	S73161	487	2	hypothetical prote
1322	5.2	62.5	T40116	490	2	hypothetical prote
1323	5.2	62.5	AC0768	492	2	probable transmemb
1324	5.2	62.5	T15502	494	2	hypothetical prote
1325	5.2	62.5	JN0539	501	1	head protein gp5 -
1326	5.2	62.5	C86263	502	2	hypothetical prote
1327	5.2	62.5	S44647	505	2	f42h10.1 protein -
1328	5.2	62.5	S52677	507	2	probable membrane
1329	5.2	62.5	AE0571	546	2	probable membrane
1330	5.2	62.5	S64332	547	2	probable membrane
1331	5.2	62.5	S64567	568	2	hypothetical prote
1332	5.2	62.5	T22928	569	1	NADH2 dehydrogenas
1333	5.2	62.5	T11478	572	2	interleukin-10 rec
1334	5.2	62.5	I56215	578	2	hypothetical prote
1335	5.2	62.5	T02596	580	2	NADH2 dehydrogenas
1336	5.2	62.5	T11451	601	2	hypothetical prote
1337	5.2	62.5	T34391	608	2	myosin-light-chain
1338	5.2	62.5	A28798	610	1	probable cellulose
1339	5.2	62.5	B95897	621	2	white homolog - hu
1340	5.2	62.5	G02068	638	2	hypothetical prote
1341	5.2	62.5	C71868	668	2	intensifier 1 prot
1342	5.2	62.5	T04073	685	2	hypothetical prote
1343	5.2	62.5	T19254	697	2	hypothetical prote
1344	5.2	62.5	S46000	704	2	probable membrane
1345	5.2	62.5	T05840	718	2	subtilisin-like pr
1346	5.2	62.5	T27937	763	2	hypothetical prote
1347	5.2	62.5	T28279	807	2	ORF MSV119 probabl
1348	5.2	62.5	G97266	815	2	mannose-1-phosphat
1349	5.2	62.5	D71027	837	2	hypothetical prote
1350	5.2	62.5	A33810	848	2	band 3 anion trans
1351	5.2	62.5	AB1658	865	2	probable membrane
1352	5.2	62.5	G96574	881	2	hypothetical prote
1353	5.2	62.5	H71719	971	2	hypothetical prote
1354	5.2	62.5	T41988	1082	2	hypothetical prote
1355	5.2	62.5	A81983	1144	2	probable DNA-direc
1356	5.2	62.5	C87691	1195	2	hypothetical prote
1357	5.2	62.5	T17242	1291	2	hypothetical prote
1358	5.2	62.5	T20642	1391	2	hypothetical prote
1359	5.2	62.5	E87998	1397	2	protein F09C3.1 [i
1360	5.2	62.5	T21172	1576	2	hypothetical prote
1361	5.2	62.5	E71410	1676	2	probable centromer
1362	5.2	62.5	T43144	1687	2	vitellogenin II pr
1363	5.2	62.5	B43963	1951	2	RNA viral polymera
1364	5.2	62.5	S13553	2150	2	hypothetical prote
1365	5.2	62	T11073	112	2	hypothetical prote
1366	5.2	62	D82954	132	2	NADH2 dehydrogenas
1367	5.2	62	E84028	174	2	hypothetical prote
1368	5.2	62	IMECB	175	1	cell-shape determi
1369	5.2	62	E97217	198	2	colicin B immunity
1370	5.2	62	G90134	201	2	uncharacterized co
1371	5.2	62	F89840	206	2	hypothetical prote
1372	5.2	62	A88656	209	2	conserved hypothet
1373	5.2	62	T32573	209	2	protein F37C4.1 [i
1374	5.2	62	B65127	225	2	hypothetical prote
1375	5.2	62	F75433	242	1	type 4 prepilin-li
1376	5.2	62	AC1332	247	2	probable phosphoes
1377	5.2	62	E70010	273	2	potassium channel
1378	5.2	62	H95943	285	2	dihydrolipoamide s
1379	5.2	62	A69838	287	2	probable sugar upt
1380	5.2	62	S36953	288	2	transcription regu
1381	5.2	62	C83356	288	2	cytochrome-c oxida
1382	5.2	62	T29189	305	2	probable permease
1383	5.2	62	T43972	306	2	hypothetical prote
1384	5.2	62	AI0209	306	2	hypothetical prote
1385	5.2	62	T41290	312	2	probable sugar ABC
1386	5.2	62	S48851	312	2	conserved hypothet
1387	5.2	62	S48849	315	2	chalcone reductase
1388	5.2	62	T24821	331	2	chalcone reductase
1389	5.2	62	AB3117	344	2	hypothetical prote
1390	5.2	62	T05987		2	hypothetical prote
1391	5.2	62	T32203	345	2	hypothetical prote
1392	5.2	62	C86408	351	2	hypothetical prote
1393	5.2	62	C98170	352	2	F3H9.12 protein -
1394	5.2	62	T42971	353	2	hypothetical prote
1395	5.2	62	A53611	360	2	hypothetical prote
1396	5.2	62	T33260	360	2	interleukin-8 rece
1397	5.2	62	B57641	363	2	hypothetical prote
1398	5.2	62	S42379	363	2	G protein-coupled
1399	5.2	62	H84111	370	2	hypothetical prote
1400	5.2	62	T05427	377	2	response regulator
1401	5.2	62	S58457	379	2	hypothetical prote
1402	5.2	62	E58851	379	2	ubiquinol-cytochro
1403	5.2	62	T11440	381	2	ubiquinol-cytochro
1404	5.2	62	C95965	383	2	probable two-compo
1405	5.2	62	B64112	398	1	bicyclomycin resis
1406	5.2	62	F72417	399	2	hypothetical prote
1407	5.2	62	JC5279	399	2	translocation prot
1408	5.2	62	AB1565	400	2	cell-division prot
1409	5.2	62	D70186	402	2	xylose operon regu
1410	5.2	62	B69338	403	2	conserved hypothet
1411	5.2	62	H72084	411	1	cbs domain protein
1412	5.2	62	A34845	432	2	protein-tyrosine-p
1413	5.2	62	T21880	432	2	hypothetical prote
1414	5.2	62	T47737	435	2	hypothetical prote
1415	5.2	62	F81367	444	2	probable transmemb
1416	5.2	62	H65054	454	2	hypothetical prote

ALIGNMENTS

RESULT 1
I38027

MLN 64 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: I38027; S60682
R;Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.;
Genomics 28, 367-376, 1995
A;Title: Identification of four novel human genes amplified and overexpressed in breast c
A;Reference number: I37080; MUID:96039245; PMID:7490069
A;Accession: I38027
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-445 <RES>
A;Cross-references: UNIPROT:Q14849; EMBL:X80198; NID:g951278; PIDN:CAA56489.1; PID:g9512
A;Note: submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Gene: MLN64

Query Match   55.6%;   Score 664; DB 2; Length 445;
Best Local Similarity 56.2%;   Pred. No. 1.2e-54;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

Qy   1 MNHLP-----EDMENAL-----TGSQSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
           |:|| |:|: | ::   :: | :::
Db   1 MSKLPELTRDLERSLPAVASLGSSLSHSQSLSSHLLPPPE--------KRRAISDV 49

Qy   52 RRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRRKVL 111
          ||||||||||||||||||||||| |:|||||| ||::::|||||:|||||
Db   50 RRTFCLFVTFDLFISLLWIIELNTNTGIRQNLEQEIIQYNPKTSFPDIFVLAFFRFSGL 109

Qy   112 ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
           :|||: : |||| | | :|::|:| ||:| : |||:::|||:||||::::|:||||||
Db   110 LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL 169

Qy   172 DFKVLPQEAEENRLLIVQDASERALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK 229
          ||||||||||||||||||| |||| : | | ||:|:|:|:::| :|::|: :|
Db   170 DFKVLPQEAEERWYLAAQVAVARGPLLFSGALSEQFYSPPESFAGSDNESDEEVAGKK 229

RESULT 2
T16170

hypothetical protein F26F4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16170
R;Fulton, L.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F26F4.
A;Reference number: Z18471
A;Accession: T16170
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-478 <FUL>
A;Cross-references: UNIPROT:Q19819; EMBL:U12964; NID:g1213452; PID:g529202; PIDN:AAA9121!
A;Experimental source: strain Bristol N2
C;Genetics:

A;Gene: CESP:F26F4.4
A;Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1

Query Match　　　　　17.1%;　Score 204; DB 2;　Length 478;
Best Local Similarity　26.5%;　Pred. No. 2.7e-11;
Matches　56;　Conservative　36;　Mismatches　73;　Indels　46;　Gaps　6;

Qy　42　GREKKGISDVRRTFCLFVTFDLLFVTLLWII----------------ELNVNGGIENTLEK 86
　　　　　　|:::|.|:|.|||:||　　||||:　　　　　　　　　　|:|:|
Db　69　GSQRIGVSKDRKRPIVITFFDTSTILLMWLLCTVTRDDDWDKVFNEINI-------FNP 121

Qy　87　EVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKL 146
　　　　　　|.||||||　　|:　　||:　.|:|.　:|.|:　|.||:　||:
Db　122　KFIRI----SLFDIVLLAVLRMLILGVVYGICLVKQWYTVAFTTLASSAVILMKVLFYFN 177

Qy　147　FSQGAFGYVLPII-SFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSD 205
　　　　　　:|:||||:||　　|:|　　　　.　||||　.|:|||:
Db　178　HSSSAVPPLLLIITSFTLCWSEFVLMPFQILPRERRYARREL---------------DGIEN 224

Qy　206　GQFYSPPPSEA-------GSEEAEBKQDSEKP 230
　　　　　　:|　|:|:|　　　.　:　|:|:
Db　225　PEFSTDDEARSNNRHRGRRQQNSGNQSEAP 255

RESULT 3
H90281
hypothetical protein dppB-1 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90281
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <KUR>
A;Cross-references: UNIPROT:Q97YQ0; GB:AE006641; NID:g13814471; PIDN:AAK41511.1; GSPDB:G
A;Genetics:
A;Gene: dppB-1

Query Match　　　　　8.6%;　Score 102.5; DB 2;　Length 348;
Best Local Similarity　23.7%;　Pred. No. 0.066;
Matches　49;　Conservative　35;　Mismatches　66;　Indels　57;　Gaps　9;

Qy　15　SQSHASLRNIHSINPTLQMARIESYEGREKKGISDVRRTFCLFVTFDLLFVTLLWIIEL 74
　　　　　　　:　|:||:|:||　　|　　　　　　　:|:
Db　46　AQFSQTLFKNAHNLNSTQIQIAVEKY--RE-----------------------SLIAAYGL 81

Qy　75　NVNGGIENTLEK-------EVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL 128
　　　　　　:　||:||:|:|:||.　　||:|　　　　||:|
Db　82　N-----QPIIDKYFIQMYNLMRFDFGTAYF-LQAPSGGSREVSSIIAYYLPN----TLLL 130

Qy　129　TTAVTSAFLLAKVILSKLFSQGAF-GYVLPIISFILAWIETWFLDFKVLPQEAEEENRLL 187
　　　　　　||:|.||　　||.|　　||||　　|:|:|||
Db　131　FTTATIVFIVAGTIIGLLSAKSKFWEKVIAIIAVIHSSIPTWWLGF-------------VL 178

Qy　188　IVQDASERAALIPGGLSDGQFYSPPES 214
　　　　　　|:|::　||:|
Db　179　IAALAYAVKVFPPGGMTS---VPPPKN 202

RESULT 4
D75080
glucose-1-phosphate thymidylyltransferase related protein PAB2433 - Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D75080
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A;Reference number: A75001
A;Accession: D75080
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-424 <KAW>
A;Cross-references: UNIPROT:Q9UZW1; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB49945
A;Experimental source: strain Orsay
C;Genetics:
C;Gene: PAB2433
C;Superfamily: Aquifex aeolicus glucose-1-phosphate thymidylyltransferase

Query Match　　　　　7.8%;　Score 93.5; DB 2;　Length 424;
Best Local Similarity　21.9%;　Pred. No. 0.59;
Matches　47;　Conservative　25;　Mismatches　72;　Indels　71;　Gaps　7;

Qy　5　PEDMENA------------------------LTGSQSHASLRNIHSINPTQLMARIESYEGRE 44
　　　　　|||:|　　　　　　　　　　　　　　|:|　|::
Db　207　PEDIKKARKLIVYTSVKGVGDGFISRHLNRKISTRISALLVEHVTPNQM--------- 255

Qy　45　KKGISDVRRTFCLFVTFDL-LFVTLLWIIELNVNG---------GIENTLEKEVMQYDY 93
　　　　　|||:|　　|||　||:|.:|:|　　　　　　　　　|:||:　|||
Db　256　-------------TIVTFLFGIFSALMNFISVPIAGILYQVSSILDGVDGEIARARMQTSK 303

Qy　94　YSSYFDIFLLAVFRFK-VLILAYAVCRLRHWWAIALTTAVTSAFL------------L 138
　　　　　:|||　　||||||　　||||
Db　304　FGGYFDSILDRYVDFTFLLILAYVSIREPLWWAIAIAMFSSAMVSYSTERFGAYCVDA 363

Qy　139　AKVI--LSKLFSQGAFGYVLPIISFILAWIETWFL 171
　　　　　|||　　|||.|:|||　|||:
Db　364　YKVIPALRKVPGKRDERIFLTMLLTLVGWIKALFL 398

RESULT 5
T43048
calcium channel alpha-1 chain - Cyanea capillata
C;Species: Cyanea capillata
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43048
R;Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.
J. Biol. Chem. 273, 22792-22799, 1998
A;Title: Cloning and functional expression of a voltage-gated calcium channel alpha1 subu
A;Reference number: Z22300; MUID:98380510; PMID:9712913
A;Accession: T43048
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1911 <JEZ>
A;Cross-references: UNIPROT:O02038; EMBL:U93075; NID:g1947095; PID:g1947096; PIDN:AAC63055
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein

Query Match　　　　　7.5%;　Score 90; DB 2;　Length 1911;
Best Local Similarity　23.5%;　Pred. No. 7.3;
Matches　43;　Conservative　33;　Mismatches　59;　Indels　48;　Gaps　9;

Qy　5　PEDMENALTGSQSHASLRNIHSINPTQLM-----ARIESYEGREKKGISDV----------- 51
　　　　　　|||:|.|:||:|:||　　　　||
Db　791　PEDVE--LGNPKSKNGTLRHMGETTSTEMSEGKEARIRPLLSELNLLKDIPDPMPPESS 848

Qy　52　--------RRTFCLFVTFDLLFVT--LLWIIELNVNGGIENTLEKEVMQYDYYSSYFDI 100
　　　　　　|||　　　||.|:　　|||
Db　849　FFIFSANNKLRYLCYRLAVNKIFINSILVLIIMSSVALAAEDPIGRDVLR-NKILGYFDI 907

Qy　101　FLLAVFRFKVLI--LAYAV---------CR------------LRHWWAIALTT-AVTSAFLLA 139
　　　　　:|:|.　:|:　　|:||　　　　　||
Db　908　FFTAMFTFEVTVKMIAFGVILHKRSFCRSFFNQLDLVIVAVSWAAIMLSRGSATSVVRIL 967

Qy　140　KVI 142
　　　　　:|:
Db　968　RVL 970

RESULT 6

T21969
hypothetical protein F38E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21969
R;Matthews, P.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19495
A;Accession: T21969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-767 <WIL>
A;Cross-references: UNIPROT:Q20170; EMBL:Z68342; PIDN:CAA92775.1; GSPDB:GN00022; CESP:F3
A;Experimental source: clone F38E11
C;Genetics:
A;Gene: CESP:F38E11.7
A;Map position: 4
A;Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1; 6

Query Match   7.2%;   Score 86.5; DB 2; Length 767;
Best Local Similarity   24.8%;   Pred. No. 5.4;
Matches   35; Conservative   22; Mismatches   49; Indels   35; Gaps   5;

Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLIL--AYAV 117
            |||| :: || | :: |||||||||||||||: :|| |||||: | |
Db   109 FDIILRSMLSFYE----DGVLITSFSETWRHYVHSFYFAIDLLAIFPFDYLLIRKTSAAF 164

Qy   118 CRLRHWW------------------AIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPI 158
            ||| : |:|: |: |||
Db   165 CRLNRFLKIYRIANFIAQSYGKLTQVTISLSKIFTACFLLFHV------NACVFYIISV 217

Qy   159 ISFILAW--IETWFLDFKVLP 177
            || || || ||||||||
Db   218 NSDTSSWDGVNATFDDDEYLP 238

RESULT 7
B81299
probable molybdopterin biosynthesis protein Cj1519 [imported] - Campylobacter jejuni (st
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 16-Aug-2004
C;Accession: B81299
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Reference number: B81299
A;Accession: B81299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <PAR>
A;Cross-references: UNIPROT:Q9PME5; GB:AL139078; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB7393
A;Experimental source: serotype O2; strain NCTC 11168
C;Genetics:
A;Gene: moeA2; Cj1519
C;Superfamily: Molybdenum cofactor molybdenum incorporation protein MoeA

Query Match   7.2%;   Score 85.5; DB 2; Length 396;
Best Local Similarity   21.0%;   Pred. No. 3.1;
Matches   47; Conservative   35; Mismatches   81; Indels   61; Gaps   9;

Qy   4 LPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLF----- 58
            | :::   : |
Db   185 LGEALENPAQIRSSNHAIANL--------------------AKNLNCDTRVFPLLKDDEK 225

Qy   59 VTFDLLFVTLLWIIELNVNGGIE----NTLEKEVMQYDYSSYFDI--------------- 100
            ||| :||| |||: : |||||||||
Db   226 ATFSTLESALQSCDILVTTGGVSMGDFDFLKKAIKEYEIIIDKADIKPGRHIKIAKANEK 285

Qy   101 FLLAV--FRFKVLILAYAVCR--LRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVL 156
            ||| : :: | ::
Db   286 FIIALPGFPYSAMVMFNLYTREILNSW--------LLQPKDYICKAFLQGSYKKKT 333

Qy   157 PIISFILAWIETWFLDFKVLPQ-EAEEENRLLIVQDASERAALI 199
            |: |: |||||||||||| ||||| |::|: :||: :|||
Db   334 PYLEPVACNIB--FKNGRILANLEGKKEGSSAIINNLNNKAALM 375

RESULT 8
A57219
Batten disease-related protein CLN3 - human
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C;Accession: A57219
R;Lerner, T.J.; Boustany, R.M.N.; Anderson, J.W.; D'Arigo, K.L.; Schlumpf, K.; Buckler, /
.E.M.; de Vos, N.; van Ommen, G.J.B.; Breuning, M.H.; Doggett, N.A.; Meincke, L.J.; Liu,
.; Mole, S.E.
Cell 82, 949-957, 1995
A;Title: Isolation of a novel gene underlying Batten disease, CLN3.
A;Reference number: A57219; MUID:96016090; PMID:7553855
A;Accession: A57219
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-438 <LER>
A;Cross-references: UNIPROT:Q13286; GB:U32680; NID:g1039422; PIDN:AAB51075.1; PID:g10394:
C;Genetics:
A;Gene: GDB:CLN3
A;Cross-references: GDB:120593; OMIM:204200
A;Map position: 16p12.1-16p11.2
C;Superfamily: CLN3 protein/Battenin/Batten disease protein/BTN1 protein
C;Keywords: membrane protein

Query Match   7.2%;   Score 85.5; DB 2; Length 438;
Best Local Similarity   25.5%;   Pred. No. 3.5;
Matches   38; Conservative   18; Mismatches   46; Indels   47; Gaps   8;

Qy   64 LFVTLLWII-----------------BLNVNGGI------ENTLEKEVMQYDYSSYFDIFLLAVFRF 108
            : || ||| : || | :|||||||||||||||:|||||:
Db   277 VFKGLLWYIVPLVVVVFABYFINQGLFELLFFWNTSLSHAQQYRWTQM---LYQAGVFAS 333

Qy   109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVVLPIISFIL----- 163
            | | || |::: ||::|||||||| WFGF-LPSIYLVFLILY 380
Db   334 R---SLRCCRIRFTWALALLQCLNLVFLLADV--------------------

Qy   164 ------AWIETWFLDFKVLPQEAEEENR 185
            |||||||||||||
Db   381 EGLLGGAAYVNT----FHNIALETSDEHR 405

RESULT 9
G70172
conserved hypothetical integral membrane protein BB0584 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70172
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70172
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-448 <KLE>
A;Cross-references: UNIPROT:O51531; GB:AE001160; GB:AE000783; NID:g2688505; PIDN:AAB9152:
A;Experimental source: strain B31

Query Match   7.1%;   Score 85; DB 2; Length 448;
Best Local Similarity   24.4%;   Pred. No. 4;
Matches   47; Conservative   28; Mismatches   64; Indels   54; Gaps   11;

Qy   50 DVRRTFCLFVTFDLLFVTL----LWIIELNVNGGIE-NTLEKEVMQYDYSS--------Y 97
            |: |: |||:   :: ||||| ||||||||||||
Db   271 DTHKYAAYSISFSIYFIFNIIHSFCISLNIMMGYEMHNSKKBIMKVAIYLSKIGLKLAF 330

```
Qy    98 FDIFPLLAVPRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVI--LSKLFSQGA---- 151
            :|:|:|:| :||  | :|||  |:||
Db   331 LTSPVLFIFSFFAPYIFYTL-KYSHLIGIILRYSSVSAFFMALAFQYLFGFFRAGASPSF 389

Qy   152 --------FGYVLPIISFILAWIETWFLDFKVLPQEABEENRILLIV-----QDASERAA 197
            |||         :||:  |:|
Db   390 GAIMEGSVTFVYTIP-IAFVLA------NYTNLPFE-------IIVFIPSLEDAIKLVV 434

Qy   198 LIPCGLSDGQFYS 210
            :|
Db   435 SLP------YFYS 441
```

RESULT 10
A41680
integral membrane protein pssA - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 06-Oct-2000
C;Accession: A41680
R;Kuge, O.; Nishijima, M.; Akamatsu, Y.
J. Biol. Chem. 266, 24184-24189, 1991
A;Title: A Chinese hamster cDNA encoding a protein essential for phosphatidylserine synt
A;Reference number: A41680; MUID:92084729; PMID:1748687
A;Accession: A41680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-471 <KUG>
A;Cross-references: GB:D10234; GB:D90468; NID:g220280; PIDN:BAA01084.1; PID:d1001553; PI
A;Superfamily: Caenorhabditis elegans hypothetical protein ZC506.3
C;Keywords: membrane protein

Query Match   7.1%; Score 84.5; DB 2; Length 471;
Best Local Similarity 24.4%; Pred. No. 4.7;
Matches   32; Conservative   22; Mismatches   38; Indels   39; Gaps   7;

```
Qy    55 FCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQY--------DYYSSYFDIFLLAV 105
            ||:|:|:|: |: ::  :  : |:|:
Db   117 FLLFLNFEQVKSLMYW-LDPNLRYA---TREADIMEYAVNCHVITWERIVSHFDIFAFGH 172

Qy   106 P---RPFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF 161
            |    :|| |||      |:||  |:|
Db   173 FWGWAMKALLIRSYGLC-----WTISITWLTELF---------------FMHLLP--NF 210

Qy   162 ILAWIETWFLD 172
            |||:||||||
Db   211 AECWWDQVILD 221
```

RESULT 11
H97002
probable integral membrane protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97002
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97002
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: UNIPROT:Q97KT1; GB:AB001437; PIDN:AAK78811.1; PID:g15023727; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0835

Query Match   7.0%; Score 83.5; DB 2; Length 352;
Best Local Similarity 19.2%; Pred. No. 4.1;
Matches   38; Conservative   35; Mismatches   50; Indels   75; Gaps   8;

```
Qy    38 ESYEGREKKGISDVRRTFCLFVTFD------------------LLFVTLLWIIEL 74
            |:|:|| |||
Db   115 EFYNVRDKKTNEDMKKLIKAYLVQNKTLNMERIVKDEQIGLSKSERIIAFLATVLLITS 174

Qy    75 NVNGGI------ENTLEKEVMQ--------------YDYYSSYFDIF---LLAVPRRKVL 111
            ||           |||    |||    :||  |:||
Db   175 VVNGAVIIRDREENTYYRYMYSPNSKFEYIFGNVYIFSYIQLFIANSLMAIFGIYIG 234

Qy   112 I-----LAYAVCRLRHWWAIALTTAVTSAF------LLAKVILSKLFSQGAFGYVLPIIS 160
            |         :||  |:||
Db   235 ISFLKMLSYGL--------ILTLVMTTFGTFIVCIFNKELYANMFSAA--------IS 276

Qy   161 FILAWIETWFLDFKVLPQ 178
            |||:||||:|:|::|
Db   277 LILSLVGGTFINYKIMPE 294
```

RESULT 12
AE0302
sugar ABC transporter, permease protein YPO2476 [imported] - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0302
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-291 <KUR>
A;Cross-references: UNIPROT:Q8ZDT0; GB:AL590842; PIDN:CAC91281.1; PID:g15980470; GSPDB:GN
C;Genetics:
A;Gene: YPO2476
C;Superfamily: inner membrane protein ugpA

Query Match   6.9%; Score 83; DB 2; Length 291;
Best Local Similarity 22.3%; Pred. No. 3.7;
Matches   44; Conservative   26; Mismatches   57; Indels   70; Gaps   10;

```
Qy    46 KGISDVRRTFCLFVFDLLFVTLLWIIELNVN--------------GGIENTL-------- 84
            |:
Db     9 KQVGSVLAASYLGYTSIFWFYPFIWLAVLSLTEWRFVGIPTFNGLNNFILVMQDPLFWKS 68

Qy    85 EKEVMQYDYSSYFDIFLLAVPRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKV--- 141
            ||      :|:|  | ||||
Db    69 MLNVMRFLMY-YLPIVFISSFLF-----AFGLQKLKHG-----RTFVALSPLLANVSSG 116

Qy   142 ------ILSKLFSQGA-------FGYVLPIIS-------FILAWIETW-------FL 171
            |||:||:|| |||
Db   117 VAYSIVFSKIFSQNGPLNTFLYDWFGFTLPWLTSPDFAMLSIALVVTWKFVGYYGLLFS 176

Qy   172 DFKVLPQB----AEEEN 184
            |:|  |
Db   177 GLNSIPKEIYSAAELDN 193
```

RESULT 13
S34960
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion
C;Species: mitochondrion Crithidia oncopelti
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34960
R;Maslov, D.A.; Horvath, A.; Gwang II, K.; Kolesnikov, A.A.
submitted to the EMBL Data Library, October 1990
A;Reference number: S34958
A;Accession: S34960
A;Molecule type: DNA
A;Residues: 1-590 <MAS>
A;Cross-references: UNIPROT:Q34192; EMBL:X56015; NID:g12879; NID:g12879; PIDN:CAA39492.1; PID:g12882
C;Genetics:

A;Gene: ND5
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match   6.9%;   Score 83;   DB 1;   Length 590;
Best Local Similarity   23.9%;   Pred. No. 8.4;
Matches 32;   Conservative 23;   Mismatches 37;   Indels 42;   Gaps   7;

Qy   55 FCLFVTF-----DLL---FVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVF 106
        : ||| :   : || ::|::| :|||::| : ||| :: : :||||||:|
Db   95 FILFYAFYYMYDLMLKRFFNIFWWFVLCMNFFI------LSYDYLTAYCGWELLGLF 146

Qy 107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWI 166
         :||: ::: ::   : | :::|: :::
Db 147 SF--FLISY-----FWYRFFALKFGFKSFFISKI------------GDVLLLSFVMTFI 187

Qy 167 ET-------WFLDF 173
             :|;|:|
Db 188 STGYGMINFYFVNF 201

RESULT 14
B29835
TraS protein - Escherichia coli plasmid pED208
C;Species: Escherichia coli
C;Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004
C;Accession: B29835
R;Finlay, B.B.; Paranchych, W.
J. Bacteriol. 166, 713-721, 1986
A;Title: Nucleotide sequence of the surface exclusion genes traS and traT from the IncF-
A;Reference number: A29835; MUID:86223783; PMID:3011738
A;Accession: B29835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <FIN>
C;Cross-references: UNIPROT:P14498
C;Genetics:
A;Genome: plasmid

Query Match   6.9%;   Score 82.5;   DB 2;   Length 186;
Best Local Similarity   23.8%;   Pred. No. 2.4;
Matches 31;   Conservative 24;   Mismatches 40;   Indels 35;   Gaps   6;

Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLL-----AVFRFKVLILAY 115
         | |||:   : :: : ||: || :|:
Db   44 FQLLFI----IFDIPINSNVR----------DYH--YFDTFVITLGSNAFFSLVFLMSTY 87

Qy 116 AVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPII---------SFILAW 165
          :|:| |:| | : |:: || : | ::
Db   88 NLVSLK----ISLGSEITEQSVLLKLVERKINSYCQFLMVVNAIVGCVLLSSGERFVAGL 143

Qy 166 IETWFLDFKV 175
          :|| :; :
Db 144 GFSWFVTYLI 153

RESULT 15
C64227
hypothetical protein homolog MG247 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C64227
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: C64227
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-239 <TIGR>
A;Cross-references: UNIPROT:P47489; GB:U39703; GB:L43967; NID:g3844835; PIDN:AAC71467.1;
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: Escherichia coli ygiH protein

Query Match   6.9%;   Score 82.5;   DB 1;   Length 239;
Best Local Similarity   21.7%;   Pred. No. 3.3;
Matches 33;   Conservative 26;   Mismatches 54;   Indels 39;   Gaps   8;

Qy   42 GREKKGISDVRRTF-------CLFVTFDLLFVTLL-WIIELNVNGGIENTLEKEVMQYD 92
         : :|| :: | ||: : |: |::|| || :: |:: |||||:|
Db   42 GSKNPGATNSMRVFGLKIGFLVAIFDAFKGFFAFLLTWIL---FRFGLQGYLTEKVQST 98

Qy   93 YYSSYFDIFLLAV------FRFK----VLILAYAVCRLRHWWAI-----ALTTAVTSA 135
         |:|: || : : ||:| ::   :::   : :: |:|:
Db   99 YFLSVLSCFAATIGHIFPLYFKFKGGKAIATTGGSLLAISLWWFLICLLIWIMITLITKY 158

Qy 136 FLLAKVILSKLFSQGAFGYVLPIISFILAWIE 167
          :|| ::|:   :|::| |:
Db 159 VSLASLITF-------FVLAVI-ILIPWLD 180

Search completed: November 16, 2005, 21:36:09
Job time : 35 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 16, 2005, 21:31:47 ; Search time 62 Seconds
(without alignments)
1932.686 Million cell updates/sec

```
Title:          US-10-063-518-14
Perfect score:  1195
Sequence:       1 MNHLPEDMENALTGSQSSHA.........EAGSEEABEKQDSEKPLLBL 234

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:        1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :    UniProt_03:*
           1: uniprot_sprot:*
           2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1*	1195	234	1	MENT_HUMAN	O95772 homo sapien
2:	1134.5	235	1	MENT_MOUSE	Q9dci3 mus musculu
3	796	227	2	Q6DI38	Q6di38 brachydanio
4	700.5	448	2	Q6DFR7	Q6dfr7 xenopus tro
5	698.5	444	2	Q6PF40	Q6pf40 xenopus lae
6	684	448	2	Q6GNT3	Q6gnt3 xenopus lae
7	664	445	1	ML64_HUMAN	Q14849 homo sapien
8	656.5	446	2	ML64_MOUSE	Q61542 mus musculu
9	612	448	2	Q8PHO3	Q6ph03 brachydanio
10	492	107	2	Q8BMP8	Q8bmp8 m mus muscu
11	348	568	2	Q7QIT3	Q7qit3 anopheles g
12	343	545	2	Q8MZH4	Q8mzh4 drosophila
13	343	583	2	Q9W145	Q9w145 drosophila
14	204	447	2	Q19819	Q19819 caenorhabdi
15	104.5	294	1	ML64_SALFO	Q902b9 salvelinus
16	102.5	348	2	Q97YQ0	Q97yq0 sulfolobus
17	93.5	424	2	Q9UZW1	Q9uzw1 pyrococcus
18	93.5	564	2	Q8HQ10	Q8hq10 thrips imag
19	91	246	2	Q8DU10	Q8du10 streptococc
20	91	525	2	Q7VFT4	Q7vft4 helicobacte
21	91	651	2	Q8DZX0	Q8dzx0 streptococc
22	91	651	2	Q8E5M0	Q8e5m0 streptococc
23	90.5	262	2	Q7NBJ4	Q7nbj4 mycoplasma
24	90	1911	2	O02038	O02038 cyanea capi
25	89.5	233	2	Q6JCT3	Q6jct3 aleurodicus
26	89.5	367	2	Q8HEH8	Q8heh8 varroa dest
27	89.5	376	2	Q6JCT6	Q6jct6 aleurodicus
28	89.5	488	2	Q840W7	Q840w7 streptococc
29	89	373	2	Q7RTB5	Q7rtb5 plasmodium
30	88.5	384	2	Q6WNV4	Q6wnv4 rana catesb
31	87	304	2	Q640E5	Q640e5 xenopus lae
32	87	7.3	610	2	Q7RRS2	Q7rrs2 plasmodium
33	87	7.3	707	2	Q8GN42	Q8gn42 xenopus lae
34	87	7.3	720	2	Q8PYM2	Q8pym2 methanosarc
35	86.5	7.2	328	2	Q7NLL9	Q7nll9 gloeobacter
36	86.5	7.2	605	2	Q7Z205	Q7z205 caenorhabdi
37	86.5	7.2	891	2	Q8JLA2	Q8jla2 ectromelia
38	86	7.2	1050	2	Q871G6	Q871g6 neurospora
39	86	7.2	1056	2	Q7S7L6	Q7s7l6 neurospora
40	85.5	7.2	174	2	P97067	P97067 salmonella
41	85.5	7.2	336	2	O95086	O95086 homo sapien
42	85.5	7.2	339	2	O95089	O95089 homo sapien
43	85.5	7.2	396	2	Q9PME5	Q9pme5 campylobact
44	85.5	7.2	438	1	CLN3_HUMAN	Q13286 homo sapien
45	85.5	7.2	473	1	PSS1_HUMAN	P48651 homo sapien
46	85.5	7.2	747	2	Q93GL8	Q93gl8 salmonella
47	85	7.1	348	2	Q9SF17	Q9sf17 arabidopsis
48	85	7.1	377	2	Q6I2C1	Q6i2c1 bacillus an
49	85	7.1	448	2	O51531	O51531 borrelia bu
50	85	7.1	797	2	Q82GJ8	Q82gj8 streptomyce
51	84.5	7.1	471	1	PSS1_CRILO	Q00576 cricetulus
52	84.5	7.1	473	1	PSS1_MOUSE	Q99lh2 mus musculu
53	84.5	7.1	487	2	Q6A0E5	Q6a0e5 mus musculu
54	84.5	7.1	892	2	Q9JF90	Q9jf90 vaccinia vi
55	84.5	7.1	1118	2	Q65U88	Q65u88 mannheimia
56	84	7.0	469	2	Q9HJK8	Q9hjk8 thermoplasm
57	84	7.0	493	2	Q7TSH7	Q7tsh7 mus musculu
58	84	7.0	1700	2	Q75JN1	Q75jn1 dictyosteli
59	83.5	7.0	275	2	Q8XIT3	Q8xit3 clostridium
60	83.5	7.0	303	2	Q6FNB8	Q6fnb8 candida gla
61	83.5	7.0	322	2	Q8LB40	Q8lb40 arabidopsis
62	83.5	7.0	352	2	Q97KT1	Q97kt1 clostridium
63	83.5	7.0	355	2	Q6KI24	Q6ki24 mycoplasma
64	83.5	7.0	380	2	Q97C55	Q97c55 thermoplasm
65	83.5	7.0	490	2	Q9CTA9	Q9cta9 mus musculu
66	83.5	7.0	599	2	Q6PCX2	Q6pcx2 mus musculu
67	83.5	7.0	662	2	Q88P20	Q88p20 pseudomonas
68	83.5	7.0	834	2	Q9JHF5	Q9jhf5 mus musculu
69	83.5	7.0	834	2	Q9JL12	Q9jl12 mus musculu
70	83.5	7.0	834	2	Q91W06	Q91w06 mus musculu
71	83.5	7.0	1034	2	Q7Z2B9	Q7z2b9 trypanosoma
72	83	6.9	238	2	Q6YR96	Q6yr96 onion yello
73	83	6.9	248	2	Q8GCS6	Q8gcs6 eubacterium
74	83	6.9	291	2	Q8ZDT0	Q8zdt0 yersinia pe
75	83	6.9	589	2	Q7TMW1	Q7tmw1 mus musculu
76	83	6.9	590	2	Q34192	Q34192 crithidia o
77	83	6.9	1056	2	Q8C2V1	Q8c2v1 mus musculu
78	83	6.9	2661	2	Q7RMS4	Q7rms4 plasmodium
79	82.5	6.9	174	2	Q6GNT3	Q6gnt3 xenopus lae
80	82.5	6.9	186	1	TRS2_ECOLI	P97231 escherichia
81	82.5	6.9	186	2	Q7BBW2	P14498 salmonella
82	82.5	6.9	239	1	Y247_MYCGE	Q7bbw2 mycoplasma
83	82.5	6.9	341	2	Q56918	P47489 yersinia en
84	82.5	6.9	367	2	Q8HCK3	Q56918 varroa dest
85	82.5	6.9	406	2	O87249	Q8hck3 lactococcus
86	82.5	6.9	419	2	O19134	O87249 oryctolagus
87	82.5	6.9	471	2	Q9QW77	O19134 cricetulus
88	82.5	6.9	510	2	Q950M6	Q9qw77 rhizophydiu
89	82.5	6.9	604	2	Q8RHJ3	Q950m6 fusobacteri
90	82.5	6.9	717	1	TRD1_ECOLI	Q8rhj3 escherichia
91	82.5	6.9	717	2	O87742	P09130 escherichia
92	82.5	6.9	891	2	O57223	O87742 vaccinia vi
93	82.5	6.9	891	2	Q6J3A9	O57223 vaccinia vi
94	82.5	6.9	891	2	Q80DW2	Q6j3a9 cowpox viru
95	82.5	6.9	892	2	Q6RZH3	Q80dw2 rabbitpox v
96	82.5	6.9	894	2	Q8QMU0	Q6rzh3 cowpox viru
97	82	6.9	1022	2	Q88V00	Q8qmu0 lactobacill
98	82	6.9	156	2	Q81501	Q88v00 hepatitis c
99	82	6.9	161	2	Q69UD2	Q81501 oryza sativ
100	82	6.9	301	2	Q8RLZ3	Q69ud2 haemophilus
101	82	6.9	303	2	Q89L18	Q8rlz3 bradyrhizob
102	82	6.9	461	2	Q6AHB8	Q89l18 leifsonia x
103	82	6.9	472	2	Q70J50	Q6ahb8 haemophilus
104	82	6.9	587	2	Q6C0H8	Q70j50 yarrowia li

No.	%	Score	Length	N	Name	Accession	Organism
105	82	6.9	589	1	RGP1_MOUSE	P46061	mus musculu
106	82	6.9	589	2	Q91YS2	Q91ys2	mus musculu
107	82	6.9	589	2	Q8C2E3	Q8c2e3	mus musculu
108	82	6.9	589	2	Q6NZB5	Q6nzb5	mus musculu
109	82	6.9	646	2	Q62PH4	Q62ph4	mus musculu
110	82	6.9	647	2	Q8PXU3	Q8pxu3	methanosarc
111	82	6.9	989	2	Q6CDE6	Q6cde6	yarrowia li
112	82	6.9	1031	2	Q8I564	Q8I564	plasmodium
113	82	6.9	1466	2	P78576	P78576	emericella
114	81.5	6.8	190	2	Q9KIA9	Q9kia9	escherichia
115	81.5	6.8	297	2	Q9B893	Q9b893	schistosoma
116	81.5	6.8	311	2	Q8CDI4	Q8cdi4	mus musculu
117	81.5	6.8	349	1	RNFD_PASMU	Q9cnp3	pasteurella
118	81.5	6.8	352	2	Q9H7E5	Q9h7e5	homo sapien
119	81.5	6.8	387	2	Q72CJ7	Q72cj7	desulfovibr
120	81.5	6.8	414	2	Q6PAH4	Q6pah4	mus musculu
121	81.5	6.8	438	2	O35934	O35934	mus musculu
122	81.5	6.8	438	2	Q8C5B1	Q8c5b1	mus musculu
123	81.5	6.8	447	2	Q7VRC0	Q7vrc0	candidatus
124	81.5	6.8	465	2	Q803C9	Q803c9	brachydanio
125	81.5	6.8	519	2	Q9NVS8	Q9nvs8	homo sapien
126	81.5	6.8	577	2	Q6PI26	Q6pi26	homo sapien
127	81.5	6.8	577	2	Q7Z748	Q7z748	homo sapien
128	81.5	6.8	645	2	Q67UQ9	Q67uq9	oryza sativ
129	81.5	6.8	716	2	Q8DLB4	Q8dlb4	synechococc
130	81.5	6.8	735	2	Q6B3Y6	Q6b3y6	escherichia
131	81.5	6.8	892	2	Q8V2P5	Q8v2p5	camelpox vi
132	81.5	6.8	892	2	Q775R6	Q775r6	camelpox vi
133	81.5	6.8	892	2	Q755K6	Q755k6	ashbya goss
134	81.5	6.8	1092	2	Q7R386	Q7r386	giardia lam
135	81.5	6.8	1480	2	Q9ZQ69	Q9zq69	arabidopsis
136	81	6.8	385	2	Q6D043	Q6d043	erwinia car
137	81	6.8	410	2	Q63ET7	Q63et7	bacillus ce
138	81	6.8	486	2	YOU1_CAEEL	P30638	caenorhabdi
139	81	6.8	520	1	YHB7_YEAST	P38745	saccharomyc
140	81	6.8	532	2	Q8XSV5	Q8xsv5	ralstonia s
141	81	6.8	805	2	Q8QRL8	Q8qrl8	hepatitis c
142	81	6.8	3010	2	P97066	P97066	salmonella
143	80.5	6.7	174	2	Q8TNE9	Q8tne9	methanosarc
144	80.5	6.7	242	2	Q9SNE5	Q9snes	arabidopsis
145	80.5	6.7	322	2	ML1A_PHOSU	P49217	phodopus su
146	80.5	6.7	353	1	Q86KR8	Q86kr8	dictyosteli
147	80.5	6.7	366	2	Q9US09	Q9us09	schizosacch
148	80.5	6.7	396	2	TNAB_PROVU	P28785	proteus vul
149	80.5	6.7	417	1	Q8Y988	Q8y988	listeria mo
150	80.5	6.7	463	2	Q72QQ4	Q72qq4	listeria mo
151	80.5	6.7	463	2	Q9G861	Q9g861	malawimonas
152	80.5	6.7	486	2	MVIN_CHLTR	Q46378	chlamydia t
153	80.5	6.7	536	1	Q7RC45	Q7rc45	plasmodium
154	80.5	6.7	548	2	Q91ME6	Q91me6	human rotav
155	80.5	6.7	599	2	YNL5_YEAST	P53925	saccharomyc
156	80.5	6.7	644	2	Q6B2V3	Q6b2v3	saccharomyc
157	80.5	6.7	644	2	Q6SIZ5	Q6siz5	escherichia
158	80.5	6.7	732	2	TRD2_ECOLI	P22708	escherichia
159	80.5	6.7	738	1	Q7AK62	Q7ak62	plasmid r10
160	80.5	6.7	738	1	VP4A_VACCC	P20642	vaccinia vi
161	80.5	6.7	891	1	VP4A_VACCV	P16715	vaccinia vi
162	80.5	6.7	891	2	Q8V4W5	Q8v4w5	monkeypox v
163	80.5	6.7	891	2	Q76ZQ5	Q76zq5	vaccinia vi
164	80.5	6.7	891	1	Q7SC49	Q7sc49	neurospora
165	80.5	6.7	1687	2	Q9ZT82	Q9zt82	arabidopsis
166	80.5	6.7	1780	2	Q9RX39	Q9rx39	deinococcus
167	80	6.7	103	2	Q8I513	Q8i513	hepatitis c
168	80	6.7	156	2	Q7YWX2	Q7ywx2	caenorhabdi
169	80	6.7	197	2	Q95KH1	Q95kh1	macaca fasc
170	80	6.7	238	2	Q6V7H6	Q6v7h6	equine arte
171	80	6.7	255	2	Q635R8	Q635r8	bacillus ce
172	80	6.7	280	2	Q731V3	Q731v3	bacillus ce
173	80	6.7	280	2	Q819H0	Q819h0	bacillus ce
174	80	6.7	280	2	Q81MM0	Q81mm0	bacillus an
175	80	6.7	280	2	Q6HEF5	Q6hef5	bacillus th
176	80	6.7	290	2	Q99UM2	Q99um2	staphylococ
177	80	6.7	290	2	Q7A5Y6	Q7a5y6	staphylococ
178	80	6.7	300	2	Q9C840	Q9c840	arabidopsis
179	80	6.7	309	1	RTM1_YEAST	P40113	saccharomyc
180	80	6.7	343	2	Q7USB9	Q7usb9	rhodopirell
181	80	6.7	347	2	Q9FFM1	Q9ffm1	arabidopsis
182	80	6.7	355	2	Q73JA5	Q73ja5	treponema d
183	80	6.7	359	2	Q7N4F8	Q7n4f8	photorhabdu
184	80	6.7	360	2	Q9H1X3	Q9h1x3	homo sapien
185	80	6.7	388	2	O58427	O58427	pyrococcus
186	80	6.7	488	2	Q650S8	Q650s8	oryza sativ
187	80	6.7	540	2	Q6FXI7	Q6fxi7	candida gla
188	80	6.7	650	2	Q699F8	Q699f8	anopheles g
189	80	6.7	661	2	Q759Y6	Q759y6	ashbya goss
190	80	6.7	680	2	Q7VH08	Q7vh08	helicobacte
191	80	6.7	700	2	Q72OZ1	Q72oz1	listeria mo
192	80	6.7	3010	2	Q9IY9	Q9iy9	hepatitis c
193	79.5	6.7	269	2	Q722B0	Q722b0	listeria mo
194	79.5	6.7	307	2	Q89NC2	Q89nc2	bradyrhizob
195	79.5	6.7	367	2	Q8ESY3	Q8esy3	oceanobacil
196	79.5	6.7	391	2	Q6TY96	Q6ty96	xiphinema a
197	79.5	6.7	438	1	CLN3_CANFA	Q29611	canis famil
198	79.5	6.7	463	2	Q92EI3	Q92e13	listeria in
199	79.5	6.7	488	2	Q6QU70	Q6qu70	aspergillus
200	79.5	6.7	491	1	VIE1_HCMVT	P03169	human cytom
201	79.5	6.7	546	1	FVR2_RAT	P60815	rattus norv
202	79.5	6.7	598	2	O51954	O51954	borrelia he
203	79.5	6.7	649	2	Q6BZ08	Q6bz08	debaryomyce
204	79.5	6.7	674	2	Q86P19	Q86p19	drosophila
205	79.5	6.7	726	2	Q9EUJ3	Q9euj3	drosophila
206	79.5	6.7	784	2	Q9VYY0	Q9vyy0	drosophila
207	79.5	6.7	784	2	Q8KDB0	Q8kdb0	chlorobium
208	79.5	6.7	3409	2	Q7SI27	Q7si27	neurospora
209	79	6.6	114	2	Q6VRR6	Q6vrr6	helicobacte
210	79	6.6	251	2	Q6MOI2	Q6moi2	methanococc
211	79	6.6	300	2	Q8OZH3	Q8ozh3	arvicanthis
212	79	6.6	308	2	Q8RGM6	Q8rgm6	fusobacteri
213	79	6.6	312	2	Q6KH29	Q6kh29	mycoplasma
214	79	6.6	323	2	Q7KSI9	Q7ksi9	drosophila
215	79	6.6	349	1	RNFD_BUCAP	Q8ka19	buchnera ap
216	79	6.6	356	2	Q7MG43	Q7mg43	vibrio vuln
217	79	6.6	375	2	Q887L9	Q887l9	pseudomonas
218	79	6.6	484	2	Q6NIE0	Q6nie0	corynebacte
219	79	6.6	770	2	Q64QD3	Q64qd3	bacteroides
220	79	6.6	1531	2	Q96L95	Q96l95	bacteroides
221	79	6.6	1679	2	Q86TB3	Q86tb3	homo sapien
222	79	6.6	3010	2	Q9J3H8	Q9j3h8	hepatitis c
223	79	6.6	3010	2	Q9QIZO	Q9qizo	hepatitis c
224	78.5	6.6	239	1	Y247_MYCPN	P75428	mycoplasma
225	78.5	6.6	269	2	Q92DL5	Q92dl5	listeria in
226	78.5	6.6	313	2	Q9L0B3	Q9l0b3	plasmodium
227	78.5	6.6	358	1	RNFD_HAEIN	Q57288	haemophilus
228	78.5	6.6	380	2	Q8A8F8	Q8a8f8	bacteroides
229	78.5	6.6	382	2	Q64V54	Q64v54	bacteroides
230	78.5	6.6	418	2	Q65LP8	Q65lp8	bacillus li
231	78.5	6.6	451	2	Q65UD5	Q65ud5	mannheimia
232	78.5	6.6	512	1	SH2A_CRIGR	P18599	cricetulus
233	78.5	6.6	666	2	Q8G1D7	Q8g1d7	brucella su
234	78.5	6.6	678	1	KUP_STRA5	Q8dzl1	streptococc
235	78.5	6.6	681	2	Q61710	Q61710	mus musculu
236	78.5	6.6	683	2	Q769F3	Q769f3	homo sapien
237	78.5	6.6	766	2	Q769F4	Q769f4	homo sapien
238	78.5	6.6	769	1	ABC9_HUMAN	Q9np78	homo sapien
239	78.5	6.6	6473	2	Q6P2Q0	Q6p2q0	homo sapien
240	78.5	6.6	188	2	Q8IKH9	Q8ikh9	plasmodium
241	78	6.5	219	2	Q81YM2	Q81ym2	bacillus an
242	78	6.5	226	2	Q8W2Y0	Q8w2y0	oryza sativ
243	78	6.5	240	2	Q7T829	Q7t829	avian infec
244	78	6.5	245	2	Q9CPF6	Q9cpf6	pasteurella
245	78	6.5	252	2	P94625	P94625	clostridium
246	78	6.5	259	2	Q6B8K2	Q6b8k2	gracilaria
247	78	6.5	321	2	Q9KD13	Q9kd13	bacillus ha
248	78	6.5	339	2	Q96XC4	Q96xc4	sulfolobus
249	78	6.5	360	2	Q8D4K9	Q8d4k9	vibrio vuln
250	78	6.5		2	Q951A3	Q951a3	tetrahymena

No.	%	pI	Len	Cnt	ID	Accession	Organism
251	78	6.5	382	2		Q97HC3	clostridium
252	78	6.5	414	2		Q8TN61	methanosarc
253	78	6.5	428	2		Q8D5Y9	vibrio vuln
254	78	6.5	431	2		Q9JRS0	actinobacil
255	78	6.5	442	2		Q7MD08	vibrio vuln
256	78	6.5	471	1	Y872_HAEIN	Q57491	haemophilus
257	78	6.5	486	2		Q6HMA8	bacillus th
258	78	6.5	545	2		Q6FSM9	candida gla
259	78	6.5	641	2		Q9LIC2	arabidopsis
260	78	6.5	650	2		Q7QGQ8	anopheles
261	78	6.5	688	2		Q98M77	rhizobium l
262	78	6.5	1297	2		Q9Y817	schizosacch
263	78	6.5	2136	1	YCF2_MARPO	P09975	marchantia
264	78	6.5	7180	1	R1AB_CVMJH	P19751	m replicase
265	77.5	6.5	176	2		Q976T7	sulfolobus
266	77.5	6.5	190	2		Q9KIA8	escherichia
267	77.5	6.5	263	2		Q73DX2	bacillus ce
268	77.5	6.5	263	2		Q8I1B3	bacillus ce
269	77.5	6.5	269	2		Q8Y8T5	listeria mo
270	77.5	6.5	270	2		Q8HIY1	perognathus
271	77.5	6.5	270	2		Q8HIY2	perognathus
272	77.5	6.5	270	2		Q8HIY3	perognathus
273	77.5	6.5	270	2		Q8HIY4	perognathus
274	77.5	6.5	294	2		Q8ET30	oceanobacil
275	77.5	6.5	299	2		Q66FT9	yersinia ps
276	77.5	6.5	299	2		Q8ZAL1	yersinia pe
277	77.5	6.5	310	2		Q8D1I6	yersinia pe
278	77.5	6.5	327	2		Q9PQG1	ureaplasma
279	77.5	6.5	328	2		Q9K686	bacillus ha
280	77.5	6.5	338	2		O42882	thermoanaer
281	77.5	6.5	365	2		Q8R770	perognathus
282	77.5	6.5	379	2		O48008	perognathus
283	77.5	6.5	392	2		Q8G7P7	bifidobacte
284	77.5	6.5	411	2		Q9P6N5	schizosacch
285	77.5	6.5	422	2		Q9HKX6	thermoplasm
286	77.5	6.5	440	2		Q9ZY23	pedinomonas
287	77.5	6.5	458	2		Q62XT1	bacillus li
288	77.5	6.5	483	2		Q9G8V8	rhodomonas
289	77.5	6.5	491	2		O28284	archaeoglob
290	77.5	6.5	491	2		Q6SX10	human cytom
291	77.5	6.5	512	2		Q8YGI2	brucella me
292	77.5	6.5	556	2		Q89J80	variola vir
293	77.5	6.5	556	2		Q89232	variola vir
294	77.5	6.5	567	2		Q7RNK0	plasmodium
295	77.5	6.5	620	2		Q8EKA1	shewanella
296	77.5	6.4	734	1	NU5C_ORYSA	P12129	oryza. sativ
297	77.5	6.4	892	1	VP4A_VARV	P33817	variola vir
298	77.5	6.4	892	2		Q9MQN0	variola vir
299	77.5	6.4	979	2		Q7MLV5	vibrio vuln
300	77.5	6.4	1476	2		Q8ST66	dictyosteli
301	77.5	6.4	1784	2		Q25377	loligo opal
302	77.5	6.4	2141	2		Q869H2	lymnaea sta
303	77	6.4	170	2		Q72UC4	leptospira
304	77	6.4	170	2		Q8F0Q4	leptospira
305	77	6.4	255	2		Q98VN5	equine arte
306	77	6.4	286	2		Q6I082	bacillus an
307	77	6.4	286	2		Q73A28	bacillus ce
308	77	6.4	332	2		Q9XTH3	caenorhabdi
309	77	6.4	353	1	ML1A_MOUSE	Q61184	mus musculu
310	77	6.4	379	2		Q8WEK6	thomomys ta
311	77	6.4	383	2		Q8TZC2	methanopyru
312	77	6.4	386	2		Q7MXQ0	porphyromon
313	77	6.4	419	2		P94949	methanopyru
314	77	6.4	423	2		Q71XS8	listeria mo
315	77	6.4	430	2		Q8U1Z6	pyrococcus
316	77	6.4	435	2		Q73RD9	treponema d
317	77	6.4	444	2		Q8NYX5	staphylococ
318	77	6.4	444	2		Q6GD70	staphylococ
319	77	6.4	490	2		O14670	homo sapien
320	77	6.4	491	2		Q9T251	phytophthor
321	77	6.4	519	2		Q9ASQ7	arabidopsis
322	77	6.4	559	2		Q9AAX4	caulobacter
323	77	6.4	590	1	NU5M_TRYBB	P04540	trypanosoma
324	77	6.4	650	2		Q8NUK4	staphylococc
325	177	6.4	650	2		Q99QZ7	staphylococc
326	77	6.4	650	2		Q7A374	staphylococc
327	77	6.4	650	2		Q6G633	staphylococc
328	77	6.4	650	2		Q6GDG1	staphylococc
329	77	6.4	722	2		Q632R1	bacillus ce
330	77	6.4	738	2		Q8L838	arabidopsis
331	77	6.4	789	1	FTSK_STAAW	Q8NWY8	staphylococc
332	77	6.4	789	2		Q6G9T7	staphylococc
333	77	6.4	836	2		Q7Z1F2	plasmodium
334	77	6.4	877	2		Q750H8	ashbya gos
335	77	6.4	991	2		Q81330	arabidopsis
336	77	6.4	1024	2		Q8IKZ6	plasmodium
337	77	6.4	1024	2		Q7Z1F1	plasmodium
338	77	6.4	1025	2		Q25693	plasmodium
339	77	6.4	1117	2		Q9M133	arabidopsis
340	77	6.4	1477	2		Q6FTR9	candida gla
341	77	6.4	1500	2		Q9ZU84	arabidopsis
342	77	6.4	3010	2		Q68788	hepatitis c
343	77	6.4	3010	2		Q81757	hepatitis c
344	77	6.4	3010	2		Q9J3G4	hepatitis c
345	77	6.4	3013	2		Q6J6P5	hepatitis c
346	77	6.4	4416	2		Q9J3F3	murine hepa
347	77	6.4	4416	2		Q9J3F8	murine hepa
348	77	6.4	7124	1	R1AB_CVM2	Q9PYA3	m replicase
349	76.5	6.4	278	2		Q8XBF0	escherichia
350	76.5	6.4	281	2		Q8SKS9	ancylostoma
351	76.5	6.4	282	2		Q92WV5	rhizobium m
352	76.5	6.4	342	2		Q7Z290	caenorhabdi
353	76.5	6.4	352	1	RNFD_SALTI		salmonella
354	76.5	6.4	352	1	RNFD_SALTY		salmonella
355	76.5	6.4	379	1	CYB_DIPOR		dipodomys o
356	76.5	6.4	379	1	CYB_DIPOR	Q9GBY7	ochotona pa
357	76.5	6.4	380	2		Q8HNI7	praomys nat
358	76.5	6.4	395	2		Q8KHK2	pseudomonas
359	76.5	6.4	415	2		Q7UB13	shigella fl
360	76.5	6.4	415	2		Q83PL5	shigella fl
361	76.5	6.4	438	1	CLN3_MOUSE	Q61124	mus musculu
362	76.5	6.4	439	2		Q64SN0	bacteroides
363	76.5	6.4	451	2		Q660T8	borrelia ga
364	76.5	6.4	453	2		Q6ZGZ4	oryza sativ
365	76.5	6.4	462	2		Q82V00	nitrosomona
366	76.5	6.4	468	1	YDBM_CAEEL	Q19084	caenorhabdi
367	76.5	6.4	490	2		Q6SX39	human cytom
368	76.5	6.4	491	2		Q6SWP6	human cytom
369	76.5	6.4	500	2		Q96ZH3	sulfolobus
370	76.5	6.4	526	1	FVR2_HUMAN	Q9UP13	homo sapien
371	76.5	6.4	528	2		Q7VP70	haemophilus
372	76.5	6.4	538	2		Q9PIV5	campylobact
373	76.5	6.4	555	2		Q8NBG4	homo sapien
374	76.5	6.4	570	2		Q7Z6J6	homo sapien
375	76.5	6.4	589	2		Q9ZLN1	helicobacte
376	76.5	6.4	614	2		Q8FWB2	brucella su
377	76.5	6.4	649	2		Q6KZL4	picrophilus
378	76.5	6.4	687	2		O74520	schizosacch
379	76.5	6.4	743	2		Q8XN80	clostridium
380	76.5	6.4	839	2		Q9I8C9	gallus gall
381	76.5	6.4	909	2		Q8T9W6	dictyosteli
382	76.5	6.4	1485	2		Q8EUA2	mycoplasma
383	76	6.4	1641	2		Q6BS27	debaryomyce
384	76	6.4	156	2		Q81504	hepatitis c
385	76	6.4	201	2		Q6MT09	mycoplasma
386	76	6.4	210	2		Q6PXL0	methanosarc
387	76	6.4	255	2		Q6V7I5	equine arte
388	76	6.4	272	2		Q8R7J2	thermoanaer
389	76	6.4	292	2		Q8ELU4	oceanobacil
390	76	6.4	325	2		Q9Z2H9	mesocricetu
391	76	6.4	342	1	NU2M_LOCMI	Q36426	locusta mig
392	76	6.4	402	2		Q21933	caenorhabdi
393	76	6.4	425	2		Q9JRS2	actinobacil
394	76	6.4	438	2		Q88HG7	pseudomonas
395	76	6.4	461	2		O85002	streptococc
396	76	6.4	474	2		Q72SX4	leptospira

No.	Accession	Organism	ID	Len	N	Score	%
397	q8f2k0	leptospira	Q8F2K0	474	2	6.4	76
398	Q852p3	perilla fru	Q852P3	519	2	6.4	76
399	Q6nxt6	homo sapien	Q6NXT6	567	2	6.4	76
400	Q7qwh6	giardia lam	Q7QWH6	616	2	6.4	76
401	Q9lz27	arabidopsis	Q9LZ27	669	2	6.4	76
402	Q6ivm6	uncultured	Q6IVM6	699	2	6.4	76
403	Q6ck04	kluyveromyc	Q6CK04	851	2	6.4	76
404	Q7nbn0	mycoplasma	Q7NBN0	931	2	6.4	76
405	Q7pvu9	anopheles g	DHX9_CABEL	1252	1	6.4	76
406	Q22307	caenorhabdi	Q7PVU9	1301	2	6.4	76
407	Q00554	oryctolagus	CFTR_RABIT	1450	1	6.4	76
408	Q9ttx9	oryctolagus	Q9TTX9	1481	2	6.4	76
409	Q96wn4	venturia in	Q96WN4	1551	2	6.4	76
410	Q18698	caenorhabdi	Q18698	1783	2	6.4	76
411	Q8mqa1	caenorhabdi	Q8MQA1	1877	2	6.4	76
412	Q7r8p2	plasmodium	Q7R8P2	2009	2	6.4	76
413	P90191	hepatitis c	P90191	3010	2	6.4	76
414	P90193	hepatitis c	P90193	3010	2	6.4	76
415	P90194	hepatitis c	P90194	3010	2	6.4	76
416	P49218	rattus norv	ML1A_RAT	156	1	6.3	75.5
417	Q66pg7	xenopus lae	Q66PG7	162	2	6.3	75.5
418	Q633a3	bacillus ce	Q633A3	220	2	6.3	75.5
419	Q9vun8	drosophila	Q9VUN8	228	2	6.3	75.5
420	Q6md11	parachlamyd	Q6MD11	231	2	6.3	75.5
421	Q6b927	gracilaria	Q6B927	244	2	6.3	75.5
422	Q7tpi3	rattus norv	Q7TPI3	247	2	6.3	75.5
423	Q63ez9	bacillus ce	Q63EZ9	248	2	6.3	75.5
424	Q6hmf5	bacillus th	Q6HMF5	248	2	6.3	75.5
425	Q63gb2	bacillus ce	Q63GB2	263	2	6.3	75.5
426	Q97pd2	streptococc	Q97PD2	263	2	6.3	75.5
427	Q81yu8	bacillus an	Q81YU8	263	2	6.3	75.5
428	Q8cyf4	streptococc	Q8CYF4	263	2	6.3	75.5
429	Q6hns6	bacillus th	Q6HNS6	263	2	6.3	75.5
430	Q66pg6	xenopus lae	Q66PG6	269	2	6.3	75.5
431	Q865k7	macropus eu	Q865K7	278	2	6.3	75.5
432	Q9kz08	streptomyce	Q9KZ08	303	2	6.3	75.5
433	Q870h5	saccharomyc	Q870H5	310	2	6.3	75.5
434	Q9esj3	rattus norv	Q9ESJ3	326	2	6.3	75.5
435	Q9kab3	vibrio chol	Q9KSB3	339	2	6.3	75.5
436	Q9qev3	human herpe	Q9QEV3	342	2	6.3	75.5
437	P58325	escherichia	RNFD_ECO57	352	1	6.3	75.5
438	P76182	escherichia	RNFD_ECOLI	352	1	6.3	75.5
439	Q8fh94	escherichia	Q8FH94	352	2	6.3	75.5
440	Q83ky5	shigella fl	Q83KY5	352	2	6.3	75.5
441	Q9xnn1	zapus trino	CYB_ZAPTR	379	1	6.3	75.5
442	Q8ays5	hyla japoni	Q8AYS5	389	2	6.3	75.5
443	Q9n4r5	caenorhabdi	Q9N4R5	397	2	6.3	75.5
444	Q6rxc2	human cytom	Q6RXC2	397	2	6.3	75.5
445	Q70nw4	strongyloid	Q70NW4	410	2	6.3	75.5
446	Q8xb33	escherichia	TNAB_ECO57	415	1	6.3	75.5
447	P23173	escherichia	TNAB_ECOLI	415	1	6.3	75.5
448	Q8fbv1	caenorhabdi	Q8FBV1	415	2	6.3	75.5
449	Q6f3c9	caenorhabdi	Q6F3C9	433	2	6.3	75.5
450	Q7s8u0	neurospora	Q7S8U0	446	2	6.3	75.5
451	P35363	mus musculu	5H2A_MOUSE	471	1	6.3	75.5
452	Q8c0k0	mus musculu	Q8C0K0	481	2	6.3	75.5
453	Q9p6j0	schizosacch	Q9P6J0	482	2	6.3	75.5
454	Q6swj1	human cytom	Q6SWJ1	491	2	6.3	75.5
455	Q6sws4	human cytom	Q6SWS4	491	2	6.3	75.5
456	Q6swv2	human cytom	Q6SWV2	491	2	6.3	75.5
457	Q6swy1	human cytom	Q6SWY1	491	2	6.3	75.5
458	O47543	chlamydomon	O47543	498	2	6.3	75.5
459	Q6chz5	yarrowia li	Q6CHZ5	501	2	6.3	75.5
460	Q91x85	mus musculu	FVR2_MOUSE	551	1	6.3	75.5
461	O25322	helicobacte	O25322	593	2	6.3	75.5
462	Q22806	caenorhabdi	Q22806	708	2	6.3	75.5
463	Q8pgm4	xanthomonas	Q8PGM4	746	2	6.3	75.5
464	Q96325	arabidopsis	Q96325	773	2	6.3	75.5
465	P92941	arabidopsis	CLCA_ARATH	775	1	6.3	75.5
466	O89154	hepatitis c	O89154	1008	2	6.3	75.5
467	Q9ut41	schizosacch	Q9UT41	1142	2	6.3	75.5
468	Q7p9s4	rickettsia	Q7P9S4	1583	2	6.3	75.5
469	Q9j3g7	hepatitis c	Q9J3G7	3010	2	6.3	75.5
470	Q6n505	rhodopseudo	Q6N505	132	2	6.3	75
471	Q81498	hepatitis c	Q81498	156	2	6.3	75
472	Q81507	hepatitis c	Q81507	156	2	6.3	75
473	Q81531	hepatitis c	Q81531	215	2	6.3	75
474	Q34238	capricornis	Q34238	218	2	6.3	75
475	Q6skb1	arthrobacte	Q6SKB1	225	2	6.3	75
476	Q6vmd0	avian infec	Q6VMD0	227	2	6.3	75
477	Q9gat3	ochotona hy	Q9GAT3	249	2	6.3	75
478	Q58763	methanococc	YD68_METJA	256	1	6.3	75
479	Q631u3	bacillus ce	Q631U3	274	2	6.3	75
480	Q9knd0	vibrio chol	Q9KND0	277	2	6.3	75
481	Q6mn43	bdellovibri	Q6MN43	294	2	6.3	75
482	Q8ret4	fusobacteri	Q8RET4	302	2	6.3	75
483	Q6cvk2	kluyveromyc	Q6CVK2	330	2	6.3	75
484	O58239	pyrococcus	O58239	371	2	6.3	75
485	Q8bw45	mus musculu	Q8BW45	373	2	6.3	75
486	P50131	sus scrofa	PE23_PIG	380	1	6.3	75
487	Q9t6r3	rana rugosa	CYB_RANRU	380	1	6.3	75
488	Q69gj2	nandus nebu	Q69GJ2	387	2	6.3	75
489	O46657	sus scrofa	O46657	407	2	6.3	75
490	Q7nrf5	chromobacte	Q7NRF5	418	2	6.3	75
491	Q6qfb8	legionella	Q6QFB8	418	2	6.3	75
492	Q6a8t1	propionibac	Q6A8T1	460	2	6.3	75
493	Q62gf6	burkholderi	Q62GF6	460	2	6.3	75
494	Q63qa3	burkholderi	Q63QA3	473	2	6.3	75
495	P24046	homo sapien	GAR1_HUMAN	488	1	6.3	75
496	Q7rw58	neurospora	Q7RW58	498	2	6.3	75
497	Q75u67	fugu rubrip	Q75U67	526	2	6.3	75
498	Q9sn21	arabidopsis	Q9SN21	543	2	6.3	75
499	Q7ns50	chromobacte	Q7NS50	649	2	6.3	75
500	O34952	bacillus su	O34952	662	2	6.3	75
501	Q7ved4	prochloroco	Q7VED4	753	2	6.3	75
502	Q98s90	guillardia	Q98S90	777	2	6.3	75
503	Q6bg55	paramecium	Q6BG55	885	2	6.3	75
504	Q8pu16	methanosarc	Q8PU16	937	2	6.3	75
505	Q82zr7	enterococcu	Q82ZR7	1008	2	6.3	75
506	O89152	hepatitis c	O89152	1008	2	6.3	75
507	O89153	hepatitis c	O89153	1008	2	6.3	75
508	O89156	hepatitis c	O89156	1131	2	6.3	75
509	Q8nat5	homo sapien	Q8NAT5	1131	2	6.3	75
510	Q8gue7	cymodocea n	Q8GUE7	1145	2	6.3	75
511	Q6fti6	candida gla	Q6FTI6	1154	2	6.3	75
512	Q6f1j1	mesoplasma	Q6F1J1	1336	2	6.3	75
513	Q95z06	trypanosoma	Q95Z06	1704	2	6.3	75
514	P32870	drosophila	CYA1_DROME	2248	1	6.3	75
515	Q9vyi7	drosophila	Q9VYI7	2248	2	6.3	75
516	Q68833	hepatitis c	Q68833	3010	2	6.3	75
517	Q9j3g2	hepatitis c	Q9J3G2	3010	2	6.3	75
518	Q9j3g5	hepatitis c	Q9J3G5	3010	2	6.3	75
519	Q9qiy7	hepatitis c	Q9QIY7	3010	2	6.3	75
520	Q9qiy8	hepatitis c	Q9QIY8	3010	2	6.3	75
521	P97068	uncultured	P97068	174	2	6.2	74.5
522	Q8eph9	oceanobacil	Q8EPH9	179	2	6.2	74.5
523	P71253	escherichia	P71253	180	2	6.2	74.5
524	Q9gat4	escherichia	Q9GAT4	227	2	6.2	74.5
525	Q9gat5	ochotona cu	Q9GAT5	227	2	6.2	74.5
526	Q9gat6	ochotona th	Q9GAT6	227	2	6.2	74.5
527	Q88wc7	ochotona pr	Q88WC7	258	2	6.2	74.5
528	Q9r9q5	lactobacill	Q9R9Q5	276	2	6.2	74.5
529	Q6wif6	rhizobium m	Q6WIF6	280	2	6.2	74.5
530	Q6seu1	synechococc	Q6SEU1	290	2	6.2	74.5
531	Q6bwd3	uncultured	Q6BWD3	298	2	6.2	74.5
532	Q8r7k6	debaryomyce	Q8R7K6	313	2	6.2	74.5
533	Q9wxs7	thermoanaer	Q9WXS7	335	2	6.2	74.5
534	P49238	thermotoga	C3X1_HUMAN	355	1	6.2	74.5
535	Q8idy2	homo sapien	Q8IDY2	364	2	6.2	74.5
536	Q766w3	plasmodium	Q766W3	377	2	6.2	74.5
537	Q6duv8	vargula hil	Q6DUV8	378	2	6.2	74.5
538	Q9gbz4	brassica na	CYB_OCHPR	379	1	6.2	74.5
539	Q8wb05	ochotona pr	Q8WB05	379	2	6.2	74.5
540	Q9b9e3	aplodontia	Q9B9E3	379	2	6.2	74.5
541	Q9lcn4	chaetodipus	Q9LCN4	392	2	6.2	74.5
542	Q94ai3	micromonosp	Q94AI3	442	2	6.2	74.5

#	6.2	Score	Accession	n	Length	Organism
543	6.2	74.5	Q65MD8	2	458	Q65md8 bacillus li
544	6.2	74.5	5H2A_RAT	1	471	P14842 rattus norv
545	6.2	74.5	Q9K5Y9	2	473	Q9k5y9 bacillus ha
546	6.2	74.5	Q6QU71	2	488	Q6qu71 aspergillus
547	6.2	74.5	O24348	2	500	O24348 sorghum bic
548	6.2	74.5	Q66GQ5	2	540	Q66gq5 arabidopsis
549	6.2	74.5	Q8N2S3	2	562	Q8n2s3 homo sapien
550	6.2	74.5	O22454	2	574	O22454 triticum ae
551	6.2	74.5	Q9VD40	2	597	Q9vd40 drosophila
552	6.2	74.5	YKR4_YEAST	2	618	P36029 saccharomyc
553	6.2	74.5	Q8VVK9	1	848	Q8vvk9 corynebacte
554	6.2	74.5	FTSK_VIBVU	2	990	Q8dm2 vibrio vuln
555	6.2	74.5	Q7Z2C1	2	1033	Q7z2c1 trypanosoma
556	6.2	74.5	Q7Z2C0	2	1034	Q7z2c0 trypanosoma
557	6.2	74.5	Q94447	2	1183	Q94447 calliphora
558	6.2	74.5	Q8T687	2	1520	Q8t687 dictyosteli
559	6.2	74.5	Q7S0S1	2	1559	Q7s0s1 neurospora
560	6.2	74.5	Q9LYS6	2	1808	Q9lys6 arabidopsis
561	6.2	74.5	Q8IKF1	2	1837	Q8ikf1 plasmodium
562	6.2	74.5	Q91AU0	2	3010	Q91au0 hepatitis c
563	6.2	74	Q8KC46	2	124	Q8kc46 chlorobium
564	6.2	74	Q81528	2	156	Q81528 hepatitis c
565	6.2	74	Q8WZ72	2	167	Q8wz72 homo sapien
566	6.2	74	Q91SA2	2	225	Q91sa2 avian infec
567	6.2	74	Q88Y70	2	230	Q88y70 lactobacill
568	6.2	74	CBS2_ARCFU	1	231	O27961 archaeoglob
569	6.2	74	O28892	2	231	O28892 archaeoglob
570	6.2	74	Q6HET1	2	238	Q6het1 bacillus th
571	6.2	74	Q66483	2	255	Q66483 equine arte
572	6.2	74	Q6CUI8	2	278	Q6cui8 kluyveromyc
573	6.2	74	POTB_MYCPN	1	286	P75058 mycoplasma
574	6.2	74	Q669G8	2	291	Q669g8 yersinia ps
575	6.2	74	Q9SM72	2	294	Q9sm72 oryza sativ
576	6.2	74	CYOE_PSEPU	1	295	Q9wwr5 pseudomonas
577	6.2	74	Q6S4M3	2	295	Q6s4m3 pseudomonas
578	6.2	74	NU2M_ASCSU	1	300	P24877 ascaris suu
579	6.2	74	PYRB_AERPE	1	312	Q9ybd4 aeropyrum p
580	6.2	74	Q9CH74	2	312	Q9ch74 lactococcus
581	6.2	74	Q710S2	2	315	Q710s2 spalax leuc
582	6.2	74	Q8M6V0	2	321	Q8m6v0 tigriopus j
583	6.2	74	Q8DVZ6	2	324	Q8dvz6 streptococc
584	6.2	74	I10S_MOUSE	1	349	mus musculu
585	6.2	74	ML1A_HUMAN	1	350	P48039 homo sapien
586	6.2	74	Q8VHM7	2	351	Q8vhm7 mus musculu
587	6.2	74	Q65U34	2	354	Q65u34 mannheimia
588	6.2	74	Q64AL9	2	361	Q64al9 uncultured
589	6.2	74	CYB_THOMO	1	379	Q8wek2 thomomys mo
590	6.2	74	O47980	2	379	O47980 thomomys bo
591	6.2	74	O48002	2	379	O48002 thomomys mo
592	6.2	74	O48003	2	379	O48003 thomomys mo
593	6.2	74	Q8WEK5	2	379	Q8wek5 thomomys ta
594	6.2	74	Q8HHJ7	2	379	Q8hhj7 thomomys bo
595	6.2	74	Q74KB0	2	380	Q74kb0 lactobacill
596	6.2	74	CYB_PSENI	1	381	Q35553 pseudantech
597	6.2	74	Q8NXC4	2	396	Q8nxc4 staphylococ
598	6.2	74	Q99V76	2	396	Q99v76 staphylococ
599	6.2	74	Q7A6D3	2	396	Q7a6d3 staphylococ
600	6.2	74	Q6GAR1	2	396	Q6gar1 staphylococ
601	6.2	74	Q6GI68	2	396	Q6gi68 staphylococ
602	6.2	74	Q6QFB9	2	418	Q6qfb9 legionella
603	6.2	74	Q6QFC5	2	418	Q6qfc5 legionella
604	6.2	74	Q6QFC7	2	418	Q6qfc7 legionella
605	6.2	74	Q9CEG6	2	442	Q9ceg6 lactococcus
606	6.2	74	Q8RBZ7	2	457	Q8rbz7 thermoanaer
607	6.2	74	Q9S2G7	2	475	Q9s2g7 streptomyce
608	6.2	74	Q9XVK0	2	487	Q9xvk0 caenorhabdi
609	6.2	74	O23384	2	493	O23384 arabidopsis
610	6.2	74	Q9EVJ7	2	503	Q9evj7 flavobacter
611	6.2	74	Q6M052	2	528	Q6m052 methanococc
612	6.2	74	Q6CKK2	2	528	Q6ckk2 kluyveromyc
613	6.2	74	Q701Q9	2	540	Q701q9 plasmodium
614	6.2	74	Q6LF33	2	540	Q6lf33 plasmodium
615	6.2	74	Q6FII6	2	581	Q6fii6 candida gla
616	6.2	74	Q9S6S6	2	650	Q9s6s6 lactococcus
617	6.2	74	Q6FNV6	2	742	Q6fnv6 candida gla
618	6.2	74	Q9AIP1	2	841	Q9aip1 carsonella
619	6.2	74	Q93U47	2	846	Q93u47 carsonella
620	6.2	74	Q8TGB2	2	892	Q8tgb2 candida alb
621	6.2	74	Q9SE99	2	1123	Q9se99 arabidopsis
622	6.2	74	Q9SPU7	2	1123	Q9spu7 arabidopsis
623	6.2	74	Q913V3	2	3010	Q913v3 hepatitis c
624	6.2	74	Q9DTE8	2	3010	Q9dte8 drosophila
625	6.2	74	Q9J3H6	2	3010	Q9j3h6 hepatitis c
626	6.2	74	Q9QIY1	2	3010	Q9qiy1 hepatitis c
627	6.2	74	Q9QIY2	2	3010	Q9qiy2 hepatitis c
628	6.2	73.5	Q9SKA6	2	120	Q9ska6 arabidopsis
629	6.2	73.5	Q92XD3	2	153	Q92xd3 rhizobium m
630	6.2	73.5	Q8ZXS3	2	180	Q8zxs3 pyrobaculum
631	6.2	73.5	P71251	2	180	P71251 escherichia
632	6.2	73.5	P71257	2	180	P71257 escherichia
633	6.2	73.5	P75018	2	180	P75018 escherichia
634	6.2	73.5	Q8DVR3	2	199	Q8dvr3 streptococc
635	6.2	73.5	YK36_AQUAE	1	216	O67827 aquifex aeo
636	6.2	73.5	Q9J0X1	2	226	Q9j0x1 avian infec
637	6.2	73.5	Q8HBP0	2	270	Q8hbp0 perognathus
638	6.2	73.5	Q8HIY6	2	270	Q8hiy6 perognathus
639	6.2	73.5	Q95L51	2	274	Q95l51 capra hircu
640	6.2	73.5	Q6Z2T3	2	298	Q6z2t3 oryza sativ
641	6.2	73.5	Q55895	2	318	Q55895 synechocyst
642	6.2	73.5	YYAD_BACSU	1	338	P37520 bacillus su
643	6.2	73.5	Q8UUW8	2	360	Q8uuw8 brachydanio
644	6.2	73.5	Q64BD6	2	367	Q64bd6 uncultured
645	6.2	73.5	CYB_PHOGR	1	367	Q35457 phoca groen
646	6.2	73.5	CYB_THOTA	1	379	O48001 thomomys ta
647	6.2	73.5	Q9G3M8	2	379	Q9g3m8 ochotona cu
648	6.2	73.5	CYB_STRPU	1	380	P15547 strongyloce
649	6.2	73.5	OPGC_SALTI	1	384	Q8z719 salmonella
650	6.2	73.5	OPGC_SALTY	1	384	Q8zq27 salmonella
651	6.2	73.5	P94442	2	385	P94442 ascaris suu
652	6.2	73.5	Q9KWU2	2	387	Q9kwu2 sphingomona
653	6.2	73.5	Q7MVX5	2	387	Q7mvx5 porphyromon
654	6.2	73.5	OXYR_MACMU	1	389	P56494 macaca mula
655	6.2	73.5	OXYR_BOVIN	1	391	P56449 bos taurus
656	6.2	73.5	Q82ZF7	2	397	Q82zf7 enterococcu
657	6.2	73.5	Q7V140	2	409	Q7v140 prochloroco
658	6.2	73.5	Q928T3	2	413	Q928t3 listeria in
659	6.2	73.5	Q8PK37	2	421	Q8pk37 xanthomonas
660	6.2	73.5	Q6D6K1	2	425	Q6d6k1 erwinia car
661	6.2	73.5	Q8GZ34	2	442	Q8gz34 arabidopsis
662	6.2	73.5	Q9XIQ7	2	442	Q9xiq7 arabidopsis
663	6.2	73.5	VIE1_HCMVA	1	491	P13202 human cytom
664	6.2	73.5	Q6SW28	2	491	Q6sw28 human cytom
665	6.2	73.5	Q7M6S4	2	491	Q7m6s4 human cytom
666	6.2	73.5	Q7RT44	2	518	Q7rt44 plasmodium
667	6.2	73.5	Q64WY6	2	523	Q64wy6 bacteroides
668	6.2	73.5	Q8VZE2	2	557	Q8vze2 arabidopsis
669	6.2	73.5	O93990	2	574	O93990 candida alb
670	6.2	73.5	Q6DFJ5	2	607	Q6dfj5 xenopus lae
671	6.2	73.5	KUP_XYLFA	1	634	Q9pc78 xylella fas
672	6.2	73.5	MUTL_BACHD	1	637	Q9kaci bacillus ha
673	6.2	73.5	APRN_ENTHI	1	640	P20301 entamoeba h
674	6.2	73.5	Q8TTH1	2	653	Q8tth1 methanosarc
675	6.2	73.5	O68468	2	661	O68468 corynebacte
676	6.2	73.5	O16531	2	731	O16531 caenorhabdi
677	6.2	73.5	Q93U53	2	846	Q93u53 carsonella
678	6.2	73.5	Q6FTY2	2	1049	Q6fty2 candida gla
679	6.2	73.5	Q9C7H5	2	1095	Q9c7h5 arabidopsis
680	6.2	73.5	Q7M006	2	1174	Q7m006 murine hepa
681	6.2	73.5	Q76G00	2	1277	Q76g00 ciona intes
682	6.2	73.5	Q7YU59	2	1287	Q7yu59 drosophila
683	6.2	73.5	Q9U5W1	2	1287	Q9u5w1 drosophila
684	6.2	73.5	Q9VL24	2	1292	Q9v124 drosophila
685	6.2	73.5	Q9AIH0	2	1292	Q9aih0 carsonella
686	6.2	73.5	Q965D3	2	1476	Q965d3 dictyosteli
687	6.2	73.5	Q8GU65	2	1545	Q8gu65 oryza sativ
688	6.2	73.5	Q6FW99	2	2666	Q6fw99 candida gla

Seq	ID	Accession	Length	Score	E	Count	Organism
689	Q9DTE6	Q9dte6	3010	73.5	6.2	2	hepatitis c
690	Q8IDK4	Q8idk4	3381	73.5	6.2	2	plasmodium
691	Q66WN5	Q66wn5	4470	73.5	6.2	2	murine hepa
692	R1AB_CVMA5	P16342	7176	73.5	6.2	1	m replicase
693	Q66WN6	Q66wn6	7178	73.5	6.2	2	murine hepa
694	Q75XA7	Q75xa7	114	73	6.1	2	helicobacte
695	Q9ZLU2	Q9zlu2	114	73	6.1	2	helicobacte
696	Q97777	Q97777	138	73	6.1	2	elephas max
697	Q64145	Q64145	140	73	6.1	2	rattus sp.
698	Q9UXB0	Q9uxb0	145	73	6.1	2	sulfolobus
699	Q7VJP1	Q7vjp1	155	73	6.1	2	helicobacte
700	Q81510	Q81510	156	73	6.1	2	hepatitis c
701	Q81522	Q81522	156	73	6.1	2	hepatitis c
702	Q81537	Q81537	156	73	6.1	2	hepatitis c
703	Q80RY8	Q80ry8	163	73	6.1	2	avian infec
704	Q72240	Q72240	220	73	6.1	2	bacillus ce
705	VME1_IBVG	Q910e2	223	73	6.1	1	avian infec
706	Q91S97	Q91s97	223	73	6.1	2	avian infec
707	Q7T9P6	Q7t9p6	226	73	6.1	2	avian infec
708	PYRF_BACCR	Q81996	238	73	6.1	1	bacillus ce
709	Q636E3	Q636e3	238	73	6.1	2	bacillus ce
710	Q73216	Q73216	238	73	6.1	2	bacillus ce
711	Q9FDU6	Q9fdu6	249	73	6.1	2	streptococc
712	P87639	P87639	255	73	6.1	2	equine arte
713	Q9YNU0	Q9ynu0	255	73	6.1	2	equine arte
714	Q7QN39	Q7qn39	261	73	6.1	2	anopheles g
715	Q7MJ52	Q7mj52	264	73	6.1	2	vibrio vuln
716	Q8DAQ9	Q8daq9	264	73	6.1	2	vibrio vuln
717	Q6TY95	Q6ty95	279	73	6.1	2	xiphinema a
718	NU2M_CAEEL	P24889	282	73	6.1	1	caenorhabdi
719	Q8NX00	Q8nx00	290	73	6.1	2	staphylococ
720	Q6G9W4	Q6g9w4	290	73	6.1	2	staphylococ
721	Q8VUQ2	Q8vuq2	295	73	6.1	2	pseudomonas
722	Q88PN3	Q88pn3	295	73	6.1	2	pseudomonas
723	Q94EJ0	Q94ej0	303	73	6.1	2	arabidopsis
724	Q8ESH3	Q8esh3	314	73	6.1	2	oceanobacil
725	Q9H6T9	Q9h6t9	322	73	6.1	2	homo sapien
726	Q99NR7	Q99nr7	326	73	6.1	2	muscardinus
727	Q8SWL8	Q8swl8	335	73	6.1	2	encephalito
728	SRG7_CAEEL	P54129	339	73	6.1	1	equine arte
729	Q9N2T2	Q9n2t2	340	73	6.1	2	caenorhabdi
730	Q7YFU0	Q7yfu0	343	73	6.1	2	myrmica sul
731	Q85AS7	Q85as7	343	73	6.1	2	uma scopari
732	Q9TD49	Q9td49	348	73	6.1	2	cynolebias
733	GHSR_MOUSE	Q99p50	364	73	6.1	1	mus musculu
734	GHSR_RAT	O08725	364	73	6.1	1	rattus norv
735	Q86NC0	Q86nc0	375	73	6.1	2	caenorhabdi
736	Q70EG4	Q70eg4	378	73	6.1	2	saccostomus
737	Q70EG5	Q70eg5	378	73	6.1	2	saccostomus
738	CYB_CRAPU	Q8wdv6	379	73	6.1	1	cratogeomys
739	Q8WDV7	Q8wdv7	379	73	6.1	2	cratogeomys
740	Q34099	Q34099	379	73	6.1	2	cratogeomys
741	Q698Q2	Q698q2	379	73	6.1	2	cynopterus
742	Q9GL20	Q9gl20	383	73	6.1	2	buchnera ap
743	Y450_BUCAP	Q9gl20	391	73	6.1	1	latimeria c
744	Q6EE99	Q6ee99	394	73	6.1	2	latimeria c
745	Q6L0J3	Q6l0j3	399	73	6.1	2	picrophilus
746	Q6KZX3	Q6kzx3	401	73	6.1	2	picrophilus
747	Q8H9B3	Q8h9b3	446	73	6.1	2	brassica ca
748	VGLM_EHV1B	P28948	450	73	6.1	1	equine herp
749	Q6DLF9	Q6dlf9	450	73	6.1	2	equid herpe
750	Q6S6V2	Q6s6v2	450	73	6.1	2	equid herpe
751	Q94307	Q94307	453	73	6.1	2	caenorhabdi
752	Q9R923	Q9r923	461	73	6.1	2	streptococc
753	Q94CI7	Q94ci7	474	73	6.1	2	arabidopsis
754	Q7MBA5	Q7mba5	487	73	6.1	2	photorhabdu
755	KCF1_HUMAN	Q9h3m0	494	73	6.1	1	homo sapien
756	Q27072	Q27072	510	73	6.1	2	taenia soli
757	Q9ZJJ5	Q9zjj5	553	73	6.1	2	helicobacte
758	Q7QZJ9	Q7qzi9	556	73	6.1	2	giardia lam
759	Q6BIQ1	Q6biq1	616	73	6.1	2	debaryomyce
760	Q86X77	Q86x77	635	73	6.1	2	homo sapien
761	Q7NBK6	Q7nbk6	643	73	6.1	2	mycoplasma
762	Q9ALX8	Q9alx8	668	73	6.1	2	burkholderi
763	Q63L61	Q63161	668	73	6.1	2	burkholderi
764	Q9VF31	Q9vf31	676	73	6.1	2	drosophila
765	FTSK_STAAN	P64164	788	73	6.1	1	staphylococ
766	FTSK_STAAN	P64165	789	73	6.1	1	staphylococ
767	Q6GHF9	Q6ghf9	832	73	6.1	2	staphylococ
768	Q7UQF9	Q7uqf9	844	73	6.1	2	rhodopirell
769	Q6KYT8	Q6kyt8	861	73	6.1	2	picrophilus
770	Q9AVX8	Q9avx8	966	73	6.1	2	guillardia
771	PKD2_MOUSE	O35245	966	73	6.1	1	mus musculu
772	Q7TSI7	Q7tsi7	971	73	6.1	2	mus musculu
773	Q8BPR6	Q8bpr6	1035	73	6.1	2	mus musculu
774	O60337	O60337	1075	73	6.1	2	homo sapien
775	Q967W1	Q967w1	1111	73	6.1	2	schistosoma
776	Q9LPE2	Q9lpe2	1127	73	6.1	2	arabidopsis
777	Q86FP2	Q86fp2	1931	73	6.1	2	caenorhabdi
778	Q9N323	Q9n323	2010	73	6.1	2	caenorhabdi
779	Q8RJY3	Q8rjy3	3010	73	6.1	2	stigmatella
780	Q7PZN7	Q7pzn7	3010	73	6.1	2	anopheles g
781	P88803	P88803	3010	73	6.1	2	hepatitis c
782	Q9J3G1	Q9j3g1	3013	73	6.1	2	hepatitis c
783	Q9J3I0	Q9j3i0	3013	73	6.1	2	hepatitis c
784	Q9QIX9	Q9qix9	6875	73	6.1	2	hepatitis c
785	Q9QIY0	Q9qiy0	156	73	6.1	2	hepatitis c
786	Q28733	Q28733	156	73	6.1	2	oryctolagus
787	Q81516	Q81516	173	72.5	6.1	2	hepatitis c
788	Q81519	Q81519	174	72.5	6.1	2	hepatitis c
789	Q9WD17	Q9wd17	180	72.5	6.1	2	equine arte
790	P97065	P97065	180	72.5	6.1	2	salmonella
791	P71252	P71252	180	72.5	6.1	2	escherichia
792	P71254	P71254	180	72.5	6.1	2	escherichia
793	P71255	P71255	180	72.5	6.1	2	escherichia
794	P71256	P71256	180	72.5	6.1	2	escherichia
795	P71258	P71258	180	72.5	6.1	2	escherichia
796	P71259	P71259	180	72.5	6.1	2	escherichia
797	P71260	P71260	191	72.5	6.1	2	escherichia
798	P71261	P71261	208	72.5	6.1	2	escherichia
799	Q8U4P0	Q8u4p0	208	72.5	6.1	2	pyrococcus
800	O63447	O63447	209	72.5	6.1	2	echinotrix
801	Q7J7L2	Q7j7l2	209	72.5	6.1	2	echinotrix
802	Q7J7L0	Q7j7l0	210	72.5	6.1	2	echinotrix
803	Q8GZ10	Q8gz10	211	72.5	6.1	2	arabidopsis
804	Q49834	Q49834	214	72.5	6.1	2	mycobacteri
805	Q7J7L9	Q7j7l9	217	72.5	6.1	2	echinotrix
806	Q7J7L3	Q7j7l3	224	72.5	6.1	2	echinotrix
807	O63950	O63950	255	72.5	6.1	2	echinotrix
808	Q9XMK7	Q9xmk7	269	72.5	6.1	2	ochotona pr
809	Q8RGE6	Q8rge6	285	72.5	6.1	2	fusobacteri
810	Q7M2C0	Q7m2c0	291	72.5	6.1	2	leishmania
811	Q8RES9	Q8res9	298	72.5	6.1	2	fusobacteri
812	Q86DD6	Q86dd6	308	72.5	6.1	2	caenorhabdi
813	O24561	O24561	309	72.5	6.1	2	zea mays (m
814	Q8R2A8	Q8r2a8	315	72.5	6.1	2	mus musculu
815	Q6N472	Q6n472	325	72.5	6.1	2	rhodopseudo
816	Q71UB1	Q71ue1	325	72.5	6.1	2	bos taurus
817	Q9LG02	Q9lg02	336	72.5	6.1	2	arabidopsis
818	OXA2_LACLA	Q9chz9	348	72.5	6.1	1	lactococcus
819	Q9CII9	Q9cii9	348	72.5	6.1	2	lactococcus
820	O17077	O17077	350	72.5	6.1	2	caenorhabdi
821	O99924	O99924	356	72.5	6.1	2	cyprinella
822	Q833B9	Q833b9	360	72.5	6.1	2	enterococcu
823	Q835L2	Q835l2	363	72.5	6.1	2	enterococcu
824	Q8FXM4	Q8fxm4	374	72.5	6.1	2	brucella su
825	Q70US3	Q70us3	379	72.5	6.1	2	lactococcus
826	Q6HGU9	Q6hgu9	379	72.5	6.1	2	bacillus th
827	Q8WMR0	Q8wmr0	379	72.5	6.1	2	ovis aries
828	CYB_OCHAL	Q9gby1	379	72.5	6.1	1	ochotona al
829	CYB_OCHCU	Q9g1b9	379	72.5	6.1	1	ochotona cu
830	CYB_OCHHI	Q9gby6	379	72.5	6.1	1	ochotona hi
831	CYB_OCHHY	Q9g6g2	379	72.5	6.1	1	ochotona hy
832	CYB_OCHKO	Q9gbz0	379	72.5	6.1	1	ochotona ko
833	CYB_OCHNB	Q9gbz2	379	72.5	6.1	1	ochotona nu
834	CYB_OCHRO	Q9gbz5	379	72.5	6.1	1	ochotona ro

No			Len	N	ID	Accession	Organism
835	72.5	6.1	379	1	CYB_OCHRU	Q9ZZU1	ochotona ru
836	72.5	6.1	379	1	CYB_OCHTH	Q9GBZ6	ochotona th
837	72.5	6.1	379	1	CYB_OCHTI	Q9GBZ7	ochotona th
838	72.5	6.1	379	2	Q70UT5	Q70UT5	ochotona pr
839	72.5	6.1	379	2	Q7ILX8	Q7ILX8	ochotona ca
840	72.5	6.1	379	2	Q85AV3	Q85AV3	chimarrogal
841	72.5	6.1	379	2	Q9G1C3	Q9G1C3	ochotona ca
842	72.5	6.1	379	2	Q9G1C4	Q9G1C4	ochotona an
843	72.5	6.1	379	2	Q9GAW7	Q9GAW7	chaetodipus
844	72.5	6.1	379	2	Q9GBY7	Q9GBY7	ochotona ca
845	72.5	6.1	379	2	Q9GBY8	Q9GBY8	ochotona hu
846	72.5	6.1	379	2	Q9GBY9	Q9GBY9	ochotona hy
847	72.5	6.1	379	2	Q9GBZ1	Q9GBZ1	ochotona la
848	72.5	6.1	379	2	Q9GBZ3	Q9GBZ3	ochotona pa
849	72.5	6.1	379	2	Q8EWI6	Q8EWI6	mycoplasma
850	72.5	6.1	387	2	Q6RKP6	Q6RKP6	human herpe
851	72.5	6.1	389	1	OXYR_HUMAN	P30559	homo sapien
852	72.5	6.1	402	2	Q8WMQ9	Q8WMQ9	ovis aries
853	72.5	6.1	428	2	Q66CF9	Q66CF9	yersinia ps
854	72.5	6.1	428	2	Q82G86	Q82G86	yersinia pe
855	72.5	6.1	442	2	Q6L0Y3	Q6L0Y3	picrophilus
856	72.5	6.1	442	2	Q6PHK5	Q6PHK5	brachydanio
857	72.5	6.1	445	2	Q6NYH8	Q6NYH8	brachydanio
858	72.5	6.1	452	2	Q9T9N6	Q9T9N6	terebratuli
859	72.5	6.1	457	2	Q6P822	Q6P822	xenopus tro
860	72.5	6.1	478	2	Q970D2	Q970D2	sulfolobus
861	72.5	6.1	491	2	Q6SWL8	Q6SWL8	human cytom
862	72.5	6.1	499	1	MVIN_AQUAE	O67658	aquifex aeo
863	72.5	6.1	505	2	Q8QRY6	Q8QRY6	pongine her
864	72.5	6.1	513	1	PACR_BOVIN	Q29627	bos taurus
865	72.5	6.1	522	2	Q23444	Q23444	caenorhabdi
866	72.5	6.1	526	2	Q6FDF6	Q6FDF6	acinetobact
867	72.5	6.1	539	2	Q7VSL1	Q7VSL1	bordetella
868	72.5	6.1	539	2	Q7W446	Q7W446	bordetella
869	72.5	6.1	539	2	Q7WFK3	Q7WFK3	bordetella
870	72.5	6.1	574	2	Q6LH28	Q6LH28	photobacter
871	72.5	6.1	614	2	Q7U5J3	Q7U5J3	synechococc
872	72.5	6.1	635	2	Q21335	Q21335	caenorhabdi
873	72.5	6.1	660	2	Q8AW53	Q8AW53	brachydanio
874	72.5	6.1	661	2	Q6G493	Q6G493	bartonella
875	72.5	6.1	662	1	KUP_STRA3	Q6G146	bartonella
876	72.5	6.1	666	2	Q64MT1	Q64MT1	bacteroides
877	72.5	6.1	671	2	Q6MCR0	Q6MCR0	parachlamyd
878	72.5	6.1	688	2	Q8EKS6	Q8EKS6	shewanella
879	72.5	6.1	696	2	Q9TU72	Q9TU72	mustela vis
880	72.5	6.1	717	2	Q7RIC0	Q7RIC0	dictyosteli
881	72.5	6.1	718	2	Q48872	Q48872	lactobacill
882	72.5	6.1	734	2	Q6ZPF2	Q6ZPF2	mus musculu
883	72.5	6.1	756	2	Q8C9E3	Q8C9E3	mus musculu
884	72.5	6.1	769	2	Q9N3Y9	Q9N3Y9	caenorhabdi
885	72.5	6.1	832	2	Q64MT1	Q64MT1	bactetoides
886	72.5	6.1	848	2	Q8VZH3	Q8VZH3	arabidopsis
887	72.5	6.1	848	2	Q9SIU2	Q9SIU2	arabidopsis
888	72.5	6.1	858	2	Q74IE5	Q74IE5	lactobacill
889	72.5	6.1	1103	2	Q753M8	Q753M8	ashbya goss
890	72.5	6.1	1304	2	Q8MNJ0	Q8MNJ0	dictyosteli
891	72.5	6.1	1357	2	Q8I7K7	Q8I7K7	caenorhabdi
892	72.5	6.1	1526	2	Q19611	Q19611	caenorhabdi
893	72.5	6.1	1548	2	Q7Q409	Q7Q409	anopheles g
894	72.5	6.1	1689	2	Q8Q2F4	Q8Q2F4	crimean-con
895	72.5	6.1	1689	2	Q991H9	Q991H9	crimean-con
896	72.5	6.1	1702	2	Q95QK2	Q95QK2	plasmodium
897	72.5	6.1	4097	2	Q7RG07	Q7RG07	caenorhabdi
898	72	6.0	114	2	Q6VRK9	Q6VRK9	helicobacte
899	72	6.0	156	2	Q81540	Q81540	hepatitis c
900	72	6.0	173	2	Q9WD22	Q9WD22	equine arte
901	72	6.0	173	2	Q9WD25	Q9WD25	equine arte
902	72	6.0	182	2	Q98BI5	Q98BI5	rhizobium l
903	72	6.0	200	2	041199	041199	porcine rep
904	72	6.0	200	2	Q9J7J6	Q9J7J6	porcine rep
905	72	6.0	209	2	Q85UI0	Q85UI0	ciona savig
906	72	6.0	225	2	Q6DTU8	Q6DTU8	avian infec
907	72	6.0	225	2	Q64FZ0	Q64FZ0	avian infec
908	72	6.0	226	2	Q7TEH2	Q7TEH2	avian infec
909	72	6.0	227	2	Q7Y6X7	Q7Y6X7	tigriopus c
910	72	6.0	239	2	O20551	O20551	ursus ameri
911	72	6.0	249	2	Q8E9R2	Q8E9R2	shewanella
912	72	6.0	254	2	Q812U8	Q812U8	bacillus ce
913	72	6.0	254	2	Q81MKO	Q81MKO	bacillus an
914	72	6.0	276	2	Q9HJV7	Q9HJV7	thermoplasm
915	72	6.0	279	2	Q9XXT1	Q9XXT1	caenorhabdi
916	72	6.0	286	2	Q6HK77	Q6HK77	bacillus th
917	72	6.0	290	2	Q6SHA6	Q6SHA6	uncultured
918	72	6.0	303	2	Q64RZ2	Q64RZ2	bacteroides
919	72	6.0	306	2	Q6HWV3	Q6HWV3	bacillus an
920	72	6.0	306	2	Q8Y980	Q8Y980	listeria mo
921	72	6.0	306	2	Q6QDA2	Q6QDA2	lepisosteus
922	72	6.0	311	2	Q8VF62	Q8VF62	mus musculu
923	72	6.0	317	2	Q9CKI6	Q9CKI6	pasteurella
924	72	6.0	320	2	Q7ZUC3	Q7ZUC3	brachydanio
925	72	6.0	323	2	Q88TJ9	Q88TJ9	lactobacill
926	72	6.0	334	2	Q88XL9	Q88XL9	lactobacill
927	72	6.0	335	2	Q9ZY32	Q9ZY32	orycteropus
928	72	6.0	338	2	Q9XTR2	Q9XTR2	caenorhabdi
929	72	6.0	339	2	Q97GD6	Q97GD6	clostridium
930	72	6.0	343	2	Q85AT6	Q85AT6	uma scopari
931	72	6.0	343	2	Q9B4H5	Q9B4H5	uma scopari
932	72	6.0	343	2	Q9TD07	Q9TD07	rachovia ma
933	72	6.0	379	1	CYB_GEOPI	Q9TEZ5	geomys pine
934	72	6.0	379	1	CYB_THOMA	Q8WEK7	thomomys ma
935	72	6.0	379	2	Q8W8K4	Q8W8K4	cratogeomys
936	72	6.0	379	2	Q8WDV3	Q8WDV3	cratogeomys
937	72	6.0	379	2	Q698Q3	Q698Q3	cratogeomys
938	72	6.0	379	2	Q7IIQ9	Q7IIQ9	cratogeomys
939	72	6.0	379	2	Q9THD6	Q9THD6	orycteropus
940	72	6.0	386	1	CYB_SARGL	O63848	sarcophyton
941	72	6.0	391	2	Q8RLY7	Q8RLY7	salmonella
942	72	6.0	391	2	Q8RLY9	Q8RLY9	salmonella
943	72	6.0	392	2	Q9LCN9	Q9LCN9	micromonosp
944	72	6.0	396	1	CYB_LAMFL	Q9TA00	lampetra fl
945	72	6.0	415	1	L52_ADE02	P03262	human adeno
946	72	6.0	415	1	L52_ADE05	P04496	human adeno
947	72	6.0	415	2	Q6VGV2	Q6VGV2	human adeno
948	72	6.0	415	2	Q71BX5	Q71BX5	human adeno
949	72	6.0	417	2	Q7M5Z2	Q7M5Z2	human adeno
950	72	6.0	418	2	Q7M633	Q7M633	human adeno
951	72	6.0	418	2	Q9NT19	Q9NT19	homo sapien
952	72	6.0	419	2	Q6QFB5	Q6QFB5	legionella
953	72	6.0	444	2	Q6QFC3	Q6QFC3	legionella
954	72	6.0	448	2	Q66IJ4	Q66IJ4	xenopus tro
955	72	6.0	448	2	Q6GKS5	Q6GKS5	staphylococ
956	72	6.0	453	1	INVX_SCHPO	042878	schizosacch
957	72	6.0	453	2	O46034	O46034	drosophila
958	72	6.0	453	2	Q99XF2	Q99XF2	staphylococ
959	72	6.0	465	2	Q7A8D9	Q7A8D9	staphylococ
960	72	6.0	468	2	Q7NWT7	Q7NWT7	chromobacte
961	72	6.0	479	2	Q9RDT2	Q9RDT2	staphylococ
962	72	6.0	497	2	Q94K50	Q94K50	saccharomyc
963	72	6.0	518	1	COQ6_YEAST	P53318	saccharomyc
964	72	6.0	523	2	Q9FVS9	Q9FVS9	arabidopsis
965	72	6.0	530	2	Q7VQX6	Q7VQX6	candidatus
966	72	6.0	552	2	Q86YB4	Q86YB4	homo sapien
967	72	6.0	553	2	Q65124	Q65124	african swi
968	72	6.0	556	2	Q6NHU7	Q6NHU7	corynebacte
969	72	6.0	562	2	Q97SL9	Q97SL9	sulfolobus
970	72	6.0	594	2	Q93YN6	Q93YN6	arabidopsis
971	72	6.0	596	2	Q6CF79	Q6CF79	yarrowia li
972	72	6.0	596	2	Q7L8K9	Q7L8K9	homo sapien
973	72	6.0	600	2	Q8R7C9	Q8R7C9	thermoanaer
974	72	6.0	610	2	O42972	O42972	schizosacch
975	72	6.0	630	2	Q84ZX2	Q84ZX2	tetraselmis
976	72	6.0	692	2	O24608	O24608	dianthus ca
977	72	6.0	696	2	Q6DD44	Q6DD44	xenopus lae
978	72	6.0	696	2	O95719	O95719	homo sapien
979	72	6.0	712	2	Q9UBH6	Q9UBH6	homo sapien
980	72	6.0	712	2	Q94EK6	Q94EK6	pisum sativ

No.	A	B	Len	Entry	Accession	Organism
981	72	6.0	716	Q7N732	Q7N732	photorhabdu
982	72	6.0	721	Q67LA6	Q67LA6	symbiobacte
983	72	6.0	736	Q7YU76	Q7YU76	drosophila
984	72	6.0	772	Q75JP4	Q75JP4	dictyosteli
985	72	6.0	788	Q8TDQ5	Q8TDQ5	homo sapien
986	72	6.0	796	Q75D67	Q75D67	ashbya goss
987	72	6.0	844	Q750H3	Q750h3	ashbya goss
988	72	6.0	878	Q9VSK2	Q9VSK2	drosophila
989	72	6.0	928	Q660E1	Q660E1	borrelia ga
990	72	6.0	1035	Q875W8	Q875W8	saccharomyc
991	72	6.0	1038	YKD3_YEAST	YKD3_YEAST	saccharomyc
992	72	6.0	1094	DPOD_PLAFK	P36097	plasmodium
993	72	6.0	1094	Q7KQL4	Q7KQL4	plasmodium
994	72	6.0	1113	Q9XKK4	Q9XKK4	caenorhabdi
995	71.5	6.0	1220	PTC1_BRARE	Q98864	brachydanio
996	71.5	6.0	1267	Q9U0U5	Q9U0U5	leishmania
997	71.5	6.0	1275	TRP_DROME	P19334	drosophila
998	71.5	6.0	1275	Q9VAE1	Q9VAE1	drosophila
999	71.5	6.0	1282	Q24809	Q24809	entamoeba h
1000	71.5	6.0	1477	Q9C250	Q9C250	neurospora
1001	71.5	6.0	1513	Q7RVU0	Q7RVU0	neurospora
1002	71.5	6.0	198	Q9QIX1	Q9QIX1	hepatitis c
1003	71.5	6.0	3010	Q9QIX2	Q9QIX2	hepatitis c
1004	71.5	6.0	161	O48242	O48242	dennyus som
1005	71.5	6.0	198	Q86X19	Q86X19	homo sapien
1006	71.5	6.0	206	Q8EYE1	Q8EYE1	leptospira
1007	71.5	6.0	210	Q37682	Q37682	trypanoplas
1008	71.5	6.0	225	VME1_IBV6	P05136	avian infec
1009	71.5	6.0	227	Q9GAT7	Q9GAT7	ochotona co
1010	71.5	6.0	229	Q7NB29	Q7NB29	mycoplasma
1011	71.5	6.0	235	O03191	O03191	monomorium
1012	71.5	6.0	237	O06251	O06251	mycobacteri
1013	71.5	6.0	237	Q7TWI5	Q7TWI5	mycobacteri
1014	71.5	6.0	246	Q8YB21	Q8YB21	brucella me
1015	71.5	6.0	254	Q8LX09	Q8LX09	laminaria d
1016	71.5	6.0	255	Q66480	Q66480	equine arte
1017	71.5	6.0	257	Q71W44	Q71W44	listeria mo
1018	71.5	6.0	266	Q8XP47	Q8XP47	clostridium
1019	71.5	6.0	270	Q8HIY5	Q8HIY5	perognathus
1020	71.5	6.0	301	Q9CJ24	Q9CJ24	lactococcus
1021	71.5	6.0	314	OR39_MOUSE	Q8VEW6	mus musculu
1022	71.5	6.0	320	Q9FAT0	Q9FAT0	vibrio para
1023	71.5	6.0	326	Q7L853	Q7L853	vibrio chol
1024	71.5	6.0	326	Q9BF45	Q9BF45	ceratotheri
1025	71.5	6.0	328	Q9BF57	Q9BF57	hylobates c
1026	71.5	6.0	328	Q89R48	Q89R48	bradyrhizob
1027	71.5	6.0	332	Q8GIP3	Q8GIP3	thermotoga
1028	71.5	6.0	334	Q9TZ00	Q9TZ00	caenorhabdi
1029	71.5	6.0	336	O79425	O79425	neomys fodi
1030	71.5	6.0	336	Q9THE4	Q9THE4	sorex radde
1031	71.5	6.0	336	Q800E8	Q800E8	tetraodon n
1032	71.5	6.0	338	Q800G2	Q800G2	tetraodon n
1033	71.5	6.0	339	Q8RD25	Q8RD25	thermoanaer
1034	71.5	6.0	341	Q98RZ1	Q98RZ1	guillardia
1035	71.5	6.0	342	VG74_HHV8	O98146	human herpe
1036	71.5	6.0	342	O90387	O90387	human herpe
1037	71.5	6.0	348	RNFD_VIBCH	Q9KT89	vibrio chol
1038	71.5	6.0	348	O99922	O99922	cyprinella
1039	71.5	6.0	355	Q8YDX2	Q8YDX2	brucella me
1040	71.5	6.0	360	Q8HIB6	Q8HIB6	callosciuru
1041	71.5	6.0	362	Q65CY4	Q65CY4	bacillus li
1042	71.5	6.0	362	Q6PDF2	Q6PDF2	mus musculu
1043	71.5	6.0	366	ML1A_SHEEP	P48040	ovis aries
1044	71.5	6.0	369	Q70VF8	Q70VF8	sorex minut
1045	71.5	6.0	375	Q6RKP7	Q6RKP7	human herpe
1046	71.5	6.0	379	CYB_OCHCO	Q95JJ5	ochotona co
1047	71.5	6.0	379	CYB_OCHPO	Q9GBY5	ochotona fo
1048	71.5	6.0	379	CYB_SORRA	O79462	sorex radde
1049	71.5	6.0	379	Q9TE55	Q9TE55	spermophilu
1050	71.5	6.0	379	CYB_SPSPA	O48007	perognathus
1051	71.5	6.0	379	Q8WEK3	Q8WEK3	thomomys ta
1052	71.5	6.0	379	Q952R3	Q952R3	glaucomys s
1053	71.5	6.0	379	Q34661	Q34661	glaucomys s

No.	Accession	Entry	C	Len	D	E	Organism
1054	Q698q0	Q698Q0	2	379	6.0	71.5	cratogeomys
1055	Q7ibw1	Q7IBW1	2	379	6.0	71.5	glaucomys s
1056	Q9tf66	Q8TF66	2	379	6.0	71.5	spermophilu
1057	Q8zxp7	Q8ZXP7	2	381	6.0	71.5	pyrobaculum
1058	O79571	O79571	2	381	6.0	71.5	mustelus ma
1059	Q6rkp4	Q6RKP4	2	382	6.0	71.5	human herpe
1060	Q9nyn8	Q9NYN8	2	383	6.0	71.5	homo sapien
1061	Q9uui8	YIY4_SCHPO	1	386	6.0	71.5	schizosacch
1062	P32306	OXYR_PIG	1	386	6.0	71.5	sus scrofa
1063	Q8rb76	Q8RB76	2	388	6.0	71.5	thermoanaer
1064	Q8sq91	Q8SQ91	2	388	6.0	71.5	nycteris th
1065	Q8sq93	Q8SQ93	2	390	6.0	71.5	nycteris gr
1066	Q90334	ITR_CATCO	1	392	6.0	71.5	catostomus
1067	Q9ah88	Q9AH88	2	407	6.0	71.5	streptococc
1068	Q6dg01	Q6DG01	2	410	6.0	71.5	brachydanio
1069	Q82ah6	Q82AH6	2	418	6.0	71.5	streptomyce
1070	Q7nke2	Q7NKE2	2	419	6.0	71.5	gloeobacter
1071	Q7v4c4	Q7V4C4	2	431	6.0	71.5	prochloroco
1072	Q66h32	Q66H32	2	435	6.0	71.5	rattus norv
1073	Q8y5e0	Q8Y5E0	2	435	6.0	71.5	listeria mo
1074	Q929p5	Q929P5	2	435	6.0	71.5	listeria in
1075	Q71xn9	Q71XN9	2	466	6.0	71.5	listeria mo
1076	Q89ii7	Q89II7	2	470	6.0	71.5	bradyrhizob
1077	Q89eq8	Q89EQ8	2	486	6.0	71.5	bradyrhizob
1078	O05351	O05351	2	489	6.0	71.5	entamoeba h
1079	Q62xj5	Q62XJ5	2	501	6.0	71.5	bacillus li
1080	Q65m56	Q65M56	2	501	6.0	71.5	bacillus li
1081	Q9xh61	Q9XH61	2	510	6.0	71.5	matricaria
1082	Q6db53	Q6DB53	2	518	6.0	71.5	erwinia car
1083	Q07423	HBX6_RICCO	1	521	6.0	71.5	ricinus com
1084	Q80g3	Q80G3	2	524	6.0	71.5	pseudomonas
1085	Q6cvf0	Q6CVF0	2	524	6.0	71.5	kluyveromyc
1086	O80905	O80905	2	536	6.0	71.5	arabidopsis
1087	Q6nhe5	Q6NHE5	2	550	6.0	71.5	corynebacte
1088	Q81f50	Q81F50	2	550	6.0	71.5	bacillus ce
1089	Q8vmk1	Q8VMK1	2	603	6.0	71.5	pseudomonas
1090	Q88im5	Q88IM5	2	603	6.0	71.5	pseudomonas
1091	Q99r71	Q99R71	2	603	6.0	71.5	staphylococ
1092	Q79zy2	Q79ZY2	2	603	6.0	71.5	staphylococ
1093	Q7a3d6	Q7A3D6	2	651	6.0	71.5	staphylococ
1094	Q6g6a7	Q6G6A7	2	663	6.0	71.5	staphylococ
1095	Q6gdn2	Q6GDN2	2	669	6.0	71.5	staphylococ
1096	Q9m2x4	Q9M2X4	2	670	6.0	71.5	arabidopsis
1097	Q66hg5	Q66HG5	2	715	6.0	71.5	rattus norv
1098	P45335	YH06_HABIN	1	725	6.0	71.5	haemophilus
1099	P46720	S1A2_RAT	1	743	6.0	71.5	rattus norv
1100	Q7z4m8	Q7Z4M8	2	814	6.0	71.5	homo sapien
1101	Q9ubk8	MTRR_HUMAN	1	838	6.0	71.5	homo sapien
1102	Q8gt52	Q8GT52	2	858	6.0	71.5	hordeum vul
1103	Q23141	Q23141	2	890	6.0	71.5	caenorhabdi
1104	Q8dg40	Q8DG40	2	1407	6.0	71	vibrio vuln
1105	Q86iy5	Q86IY5	2	1509	6.0	71	dictyosteli
1106	O76024	WFS1_HUMAN	1	2837	6.0	71	homo sapien
1107	Q03100	CYAA_DICDI	1	2923	6.0	71.5	dictyosteli
1108	Q6rcs2	Q6RCS2	2	3010	6.0	71	clona savig
1109	Q6x3j2	Q6X3J2	2	3589	6.0	71	pseudomonas
1110	Q9hcu4	CLR2_HUMAN	1	5303	6.0	71	homo sapien
1111	Q68949	Q68949	2	150	5.9	71	hepatitis c
1112	Q6lf63	Q6LF63	2	171	5.9	71	plasmodium
1113	Q9v628	Q9V628	2	173	5.9	71	drosophila
1114	O25269	O25269	2	188	5.9	71	helicobacte
1115	Q82zc0	Q82ZC0	2	195	5.9	71	enterococcu
1116	Q8u3q3	Q8U3Q3	2	199	5.9	71	pyrococcus
1117	Q9wd21	Q9WD21	2	200	5.9	71	equine arte
1118	O46635	5H2A_CANFA	1	219	5.9	71	canis famil
1119	Q6mtk4	Q6MTK4	2	223	5.9	71	mycoplasma
1120	Q8thm3	Q8THM3	2	199	5.9	71	methanosarc
1121	Q85ju8	Q85JU8	2	200	5.9	71	ceratobaeus
1122	Q9j7j9	Q9J7J9	2	214	5.9	71	porcine rep
1123	Q93id2	Q93ID2	2	219	5.9	71	drosophila
1124	Q91nk5	Q91NK5	2	223	5.9	71	staphylococ
1125	Q91nk6	Q91NK6	2	223	5.9	71	avian infec
1126	Q91s95	Q91S95	2	223	5.9	71	avian infec

No.	Score	pI	Len	n	ID Name	Accession	Organism
1127	71	5.9	223	2	Q91S96	Q91S96	avian infec
1128	71	5.9	223	2	Q91SA3	Q91SA3	avian infec
1129	71	5.9	225	1	VME1_IBVK	P12649	avian infec
1130	71	5.9	225	2	Q6R4F1	Q6R4F1	avian infec
1131	71	5.9	225	2	Q7TEG9	Q7TEG9	avian infec
1132	71	5.9	226	2	Q7T405	Q7T405	avian infec
1133	71	5.9	234	2	Q9F6V0	Q9F6V0	bacteroides
1134	71	5.9	238	1	PYRF_BACAN		bacillus an
1135	71	5.9	238	2	Q9T4G5	Q9T4G5	phlebotomus
1136	71	5.9	238	2	Q9TEW9	Q9TEW9	phlebotomus
1137	71	5.9	238	2	Q9XMR3	Q9XMR3	phlebotomus
1138	71	5.9	238	2	Q9XMR4	Q9XMR4	phlebotomus
1139	71	5.9	242	2	Q639U8	Q639U8	bacillus ce
1140	71	5.9	243	2	Q34969	Q34969	myrmecia ba
1141	71	5.9	244	2	Q74HS0	Q74HS0	lactobacill
1142	71	5.9	250	2	Q9KVQ3	Q9KVQ3	vibrio chol
1143	71	5.9	255	2	Q66484	Q66484	equine arte
1144	71	5.9	258	2	Q9PP98	Q9PP98	campylobact
1145	71	5.9	266	2	Q6W249	Q6W249	rhizobium s
1146	71	5.9	277	2	Q70NW1	Q70NW1	strongyloid
1147	71	5.9	279	2	Q7NBM0	Q7NBM0	mycoplasma
1148	71	5.9	281	2	Q8SK19	Q8SK19	necator ame
1149	71	5.9	286	2	Q63CT1	Q63CT1	bacillus ce
1150	71	5.9	289	2	Q8HZF2	Q8HZF2	macaca sp.
1151	71	5.9	290	1	CB4A_ARATH	Q07473	arabidopsis
1152	71	5.9	295	2	Q8P0V2	Q8P0V2	streptococc
1153	71	5.9	295	2	Q99ZG3	Q99ZG3	streptococc
1154	71	5.9	295	2	Q7CN71	Q7CN71	streptococc
1155	71	5.9	308	1	SRV1_CAEEL	P46564	caenorhabdi
1156	71	5.9	310	1	Y160_BUCAP		buchnera ap
1157	71	5.9	325	2	Q99NR9	Q99NR9	tamias stri
1158	71	5.9	343	2	Q7YFU4	Q7YFU4	myrmica kar
1159	71	5.9	345	2	O78911	O78911	anolis occu
1160	71	5.9	361	2	Q98PJ1	Q98PJ1	mycoplasma
1161	71	5.9	374	2	Q71EA5	Q71EA5	galerella s
1162	71	5.9	379	1	CYB_CRATY	Q8WDU1	cratogeomys
1163	71	5.9	379	1	CYB_THOUM	O47979	thomomys um
1164	71	5.9	379	2	O47981	O47981	thomomys bo
1165	71	5.9	379	2	Q8W7H1	Q8W7H1	thomomys ma
1166	71	5.9	379	2	Q698P7	Q698P7	cratogeomys
1167	71	5.9	379	2	Q698P9	Q698P9	cratogeomys
1168	71	5.9	379	2	Q6QX63	Q6QX63	ursus thibe
1169	71	5.9	379	2	Q9TF00	Q9TF00	geomys burs
1170	71	5.9	379	2	Q9TF03	Q9TF03	geomys brev
1171	71	5.9	380	2	O03396	O03396	acomys sp.
1172	71	5.9	380	2	O03397	O03397	acomys sp.
1173	71	5.9	380	2	Q6E3J7	Q6E3J7	thomomys bo
1174	71	5.9	380	2	Q9T502	Q9T502	geomys brev
1175	71	5.9	380	2	Q9T576	Q9T576	acomys sp.
1176	71	5.9	380	2	Q9T577	Q9T577	acomys sp.
1177	71	5.9	380	2	Q8EMJ1	Q8EMJ1	oceanobacil
1178	71	5.9	381	1	CYB_PHACL	Q35409	phascogale
1179	71	5.9	391	2	Q8RLY8	Q8RLY8	salmonella
1180	71	5.9	391	2	Q8RSF4	Q8RSF4	salmonella
1181	71	5.9	391	2	Q9CGL8	Q9CGL8	lactococcus
1182	71	5.9	401	2	Q850S5	Q850S5	oryza sativ
1183	71	5.9	403	2	Q8ZPR2	Q8ZPR2	salmonella
1184	71	5.9	409	2	Q9F2J6	Q9F2J6	streptomyce
1185	71	5.9	416	2	Q9ABC8	Q9ABC8	caulobacter
1186	71	5.9	418	2	Q8Y5H6	Q8Y5H6	listeria mo
1187	71	5.9	418	2	Q6QFB6	Q6QFB6	legionella
1188	71	5.9	418	2	Q6QFC0	Q6QFC0	legionella
1189	71	5.9	418	2	Q6QFC1	Q6QFC1	legionella
1190	71	5.9	418	2	Q6QFC2	Q6QFC2	legionella
1191	71	5.9	418	2	Q6QFC4	Q6QFC4	legionella
1192	71	5.9	418	2	Q6QFC6	Q6QFC6	legionella
1193	71	5.9	419	2	Q95Q81	Q95Q81	caenorhabdi
1194	71	5.9	423	2	Q6I5Y4	Q6I5Y4	oryza sativ
1195	71	5.9	438	2	Q96ZK3	Q96ZK3	sulfolobus
1196	71	5.9	438	2	P91683	P91683	drosophila
1197	71	5.9	442	2	Q9SNW3	Q9SNW3	vernicia fo
1198	71	5.9	448	2	Q9F992	Q9F992	buchnera ap
1199	71	5.9	451				homo sapien

No.	Score	pI	Len	n	ID Name	Accession	Organism
1200	71	5.9	470	1	5H2A_PIG	P50129	sus scrofa
1201	71	5.9	471	1	5H2A_HUMAN	P28223	homo sapien
1202	71	5.9	472	2	Q6KI36	Q6KI36	mycoplasma
1203	71	5.9	480	2	Q73CA7	Q73CA7	bacillus ce
1204	71	5.9	485	2	Q9CLJ7	Q9CLJ7	pasteurella
1205	71	5.9	489	2	Q8SHR0	Q8SHR0	trichoderma
1206	71	5.9	492	2	Q7N9D9	Q7N9D9	photorhabdu
1207	71	5.9	545	1	SOA1_RAT	O70536	rattus norv
1208	71	5.9	546	1	MUP3_YEAST	P38734	saccharomyc
1209	71	5.9	548	2	Q8I3H5	Q8I3H5	plasmodium
1210	71	5.9	554	2	Q8AUN9	Q8AUN9	fugu rubrip
1211	71	5.9	563	1	YAS8_SCHPO	Q10144	schizosacch
1212	71	5.9	564	1	S229_MOUSE	Q9WTN6	mus musculu
1213	71	5.9	564	2	Q6F1V1	Q6F1V1	mesoplasma
1214	71	5.9	576	1	OCT1_CAEEL	Q9U539	caenorhabdi
1215	71	5.9	584	1	LYTS_STAAU	Q53705	staphylococ
1216	71	5.9	615	2	Q7R9S0	Q7R9S0	plasmodium
1217	71	5.9	620	2	Q9ZZP7	Q9ZZP7	cyanidiosch
1218	71	5.9	631	2	Q8IW20	Q8IW20	homo sapien
1219	71	5.9	672	2	Q650E2	Q650E2	bacteroides
1220	71	5.9	676	2	O04521	O04521	arabidopsis
1221	71	5.9	701	2	Q8EWL9	Q8EWL9	mycoplasma
1222	71	5.9	762	2	Q8ML23	Q8ML23	drosophila
1223	71	5.9	788	2	Q9ZJB7	Q9ZJB7	helicobacte
1224	71	5.9	826	2	Q8TQX6	Q8TQX6	methanosarc
1225	71	5.9	885	2	Q75BG1	Q75BG1	ashbya goss
1226	71	5.9	913	2	O13099	O13099	cyanidiosch
1227	71	5.9	913	2	Q6DCC0	Q6DCC0	xenopus lae
1228	71	5.9	964	2	Q7SCL0	Q7SCL0	neurospora
1229	71	5.9	1021	2	Q65QR6	Q65QR6	mannheimia
1230	71	5.9	1239	2	Q6CBA1	Q6CBA1	yarrowia li
1231	71	5.9	1242	2	Q7T9B1	Q7T9B1	human cytom
1232	71	5.9	1409	2	Q7XW92	Q7XW92	oryza sativ
1233	71	5.9	2304	2	Q9BMQ4	Q9BMQ4	blattella g
1234	71	5.9	2423	2	O77393	O77393	plasmodium
1235	71	5.9	2681	2	Q95V80	Q95V80	strongyloce
1236	71	5.9	3010	2	Q68285	Q68285	hepatitis c
1237	71	5.9	3010	2	Q81541	Q81541	hepatitis c
1238	71	5.9	3010	2	Q81825	Q81825	hepatitis c
1239	71	5.9	3010	2	Q9DTE5	Q9DTE5	hepatitis c
1240	70.5	5.9	145	2	Q65G39	Q65G39	bacillus li
1241	70.5	5.9	203	1	BCRC_BACLI	P42334	bacillus li
1242	70.5	5.9	206	2	Q72LX2	Q72LX2	leptospira
1243	70.5	5.9	208	2	Q6BHB0	Q6BHB0	debaryomyce
1244	70.5	5.9	213	2	Q98E85	Q98E85	rhizobium l
1245	70.5	5.9	214	2	Q6GK20	Q6GK20	staphylococ
1246	70.5	5.9	216	2	Q6VRP1	Q6VRP1	helicobacte
1247	70.5	5.9	226	2	O03371	O03371	dipodomys o
1248	70.5	5.9	235	2	Q6B4U8	Q6B4U8	ovis aries
1249	70.5	5.9	235	2	Q6DHQ1	Q6DHQ1	brachydanio
1250	70.5	5.9	266	2	O74888	O74888	schizosacch
1251	70.5	5.9	266	2	Q8U854	Q8U854	agrobacteri
1252	70.5	5.9	278	2	Q85HQ3	Q85HQ3	cooperia on
1253	70.5	5.9	279	2	Q8YMV2	Q8YMV2	anabaena sp
1254	70.5	5.9	283	2	Q9AZ90	Q9AZ90	lactobacill
1255	70.5	5.9	285	2	Q7S2B8	Q7S2B8	neurospora
1256	70.5	5.9	290	2	Q6SGH2	Q6SGH2	uncultured
1257	70.5	5.9	291	2	Q37789	Q37789	helianthus
1258	70.5	5.9	292	2	O746W1	O746W1	geobacter s
1259	70.5	5.9	310	2	Q65VD8	Q65VD8	mannheimia
1260	70.5	5.9	312	2	Q6CEC0	Q6CEC0	yarrowia li
1261	70.5	5.9	315	2	Q9JK65	Q9JK65	rattus norv
1262	70.5	5.9	320	2	Q7N0S0	Q7N0S0	photorhabdu
1263	70.5	5.9	326	2	Q9BF39	Q9BF39	manis penta
1264	70.5	5.9	326	2	Q9BF58	Q9BF58	macaca mula
1265	70.5	5.9	335	2	Q9ZY31	Q9ZY31	elephantulu
1266	70.5	5.9	336	2	Q9THE3	Q9THE3	sorex pacif
1267	70.5	5.9	339	2	Q7PB28	Q7PB28	rickettsia
1268	70.5	5.9	340	2	Q55632	Q55632	synechocyst
1269	70.5	5.9	343	2	Q7Y7B1	Q7Y7B1	myrmica hir
1270	70.5	5.9	343	2	Q7Y7S5	Q7Y7S5	myrmica sab
1271	70.5	5.9	343	2	Q7YFU5	Q7YFU5	myrmica hel
1272	70.5	5.9	350	2	Q9Y370	Q9Y370	homo sapien

No.	%1	%2	Len	Accession	ID	N	Organism
1273	70.5	5.9	351	O97774	O97774	2	felis silve
1274	70.5	5.9	352	Q98R08	Q98R08	2	mycoplasma
1275	70.5	5.9	353	Q7TN44	Q7TN44	2	rattus norv
1276	70.5	5.9	356	Q9GCR9	Q9GCR9	2	glaucomys v
1277	70.5	5.9	360	Q8HIB8	Q8HIB8	2	callosciuru
1278	70.5	5.9	360	Q8HIC3	Q8HIC3	2	callosciuru
1279	70.5	5.9	361	Q9N4V8	Q9N4V8	2	caenorhabdi
1280	70.5	5.9	363	Q9K337	Q9K337	2	bacillus ce
1281	70.5	5.9	363	Q7BYC0	Q7BYC0	2	bacillus ce
1282	70.5	5.9	366	Q6TTN3	Q6TTN3	2	homo sapien
1283	70.5	5.9	369	Q70VB2	Q70VB2	2	sorex volnu
1284	70.5	5.9	370	Q6VPS4	Q6VPS4	2	canis famil
1285	70.5	5.9	373	Q7RFS0	Q7RFS0	2	plasmodium
1286	70.5	5.9	373	Q6JT34	Q6JT34	2	heptathela
1287	70.5	5.9	379	CYB_GLAVO	CYB_GLAVO	1	glaucomys v
1288	70.5	5.9	379	O48009	O48009	2	dipodomys a
1289	70.5	5.9	379	O48364	O48364	2	thomomys bo
1290	70.5	5.9	379	Q8LWU4	Q8LWU4	2	macroscelid
1291	70.5	5.9	379	Q8W9L6	Q8W9L6	2	glaucomys v
1292	70.5	5.9	379	Q85RV3	Q85RV3	2	muntiacus c
1293	70.5	5.9	379	Q9GAV5	Q9GAV5	2	dipodomys s
1294	70.5	5.9	379	Q9GAV6	Q9GAV6	2	dipodomys s
1295	70.5	5.9	379	Q9GAV7	Q9GAV7	2	dipodomys o
1296	70.5	5.9	379	Q9GAV9	Q9GAV9	2	dipodomys e
1297	70.5	5.9	379	Q9GAW1	Q9GAW1	2	dipodomys s
1298	70.5	5.9	379	Q9GAW5	Q9GAW5	2	dipodomys e
1299	70.5	5.9	379	Q9GBY3	Q9GBY3	2	ochotona da
1300	70.5	5.9	379	Q9TEZ7	Q9TEZ7	2	geomys burs
1301	70.5	5.9	382	Q9HIJ9	Q9HIJ9	2	thermoplasm
1302	70.5	5.9	386	Q6RKP3	Q6RKP3	2	human herpe
1303	70.5	5.9	387	T2C_PARTE	T2C_PARTE	1	paramecium
1304	70.5	5.9	389	MTR_BUFMA	MTR_BUFMA	1	bufo marinu
1305	70.5	5.9	390	PE23_HUMAN	PE23_HUMAN	1	homo sapien
1306	70.5	5.9	393	O00326	O00326	2	homo sapien
1307	70.5	5.9	394	Q8X1V7	Q8X1V7	2	coriolus ve
1308	70.5	5.9	402	O00325	O00325	2	homo sapien
1309	70.5	5.9	403	Q9KGY1	Q9KGY1	2	mycoplasma
1310	70.5	5.9	414	Q6Z9G4	Q6Z9G4	2	oryza sativ
1311	70.5	5.9	416	Q6VPS5	Q6VPS5	2	canis famil
1312	70.5	5.9	420	Q7BR79	Q7BR79	2	aeromonas p
1313	70.5	5.9	423	O58964	O58964	2	pyrococcus
1314	70.5	5.9	424	Q7VF09	Q7VF09	2	helicobacte
1315	70.5	5.9	436	Q6BUT5	Q6BUT5	2	debaryomyce
1316	70.5	5.9	440	CAPE_STAAU	CAPE_STAAU	1	staphylococ
1317	70.5	5.9	452	O83C47	O83C47	2	coxiella bu
1318	70.5	5.9	460	Q7VIT8	Q7VIT8	2	helicobacte
1319	70.5	5.9	470	Q6SED7	Q6SED7	2	lactobacill
1320	70.5	5.9	470	Q65PQ0	Q65PQ0	2	lactobacill
1321	70.5	5.9	472	Q9LCN5	Q9LCN5	2	micromonosp
1322	70.5	5.9	472	Q8YC07	Q8YC07	2	brucella me
1323	70.5	5.9	496	O25600	O25600	2	helicobacte
1324	70.5	5.9	496	Q8CQ64	Q8CQ64	2	staphylococ
1325	70.5	5.9	500	Q8EQ1	Q8EQ1	2	oceanobacil
1326	70.5	5.9	508	Q7RQY6	Q7RQY6	2	plasmodium
1327	70.5	5.9	521	CYOA_HAEIN	CYOA_HAEIN	1	haemophilus
1328	70.5	5.9	536	MVIN_CHLMU	MVIN_CHLMU	1	chlamydia m
1329	70.5	5.9	556	Q22109	Q22109	2	caenorhabdi
1330	70.5	5.9	556	Q7VH12	Q7VH12	2	helicobacte
1331	70.5	5.9	558	Q6EIC5	Q6EIC5	2	perkinsus m
1332	70.5	5.9	574	RFT1_YEAST	RFT1_YEAST	1	saccharomyc
1333	70.5	5.9	585	Q7RIV4	Q7RIV4	2	giardia lam
1334	70.5	5.9	598	S6A1_MUSCO	S6A1_MUSCO	1	mus cooki
1335	70.5	5.9	599	S6A1_MOUSE	S6A1_MOUSE	1	mus musculu
1336	70.5	5.9	599	S6A1_RAT	S6A1_RAT	1	rattus norv
1337	70.5	5.9	599	Q8N4K8	Q8N4K8	2	homo sapien
1338	70.5	5.9	633	Q7QS02	Q7QS02	2	giardia lam
1339	70.5	5.9	641	Q7PMH7	Q7PMH7	2	anopheles g
1340	70.5	5.9	658	Q7ZUF5	Q7ZUF5	2	brachydanio
1341	70.5	5.9	662	T9S2_MOUSE	T9S2_MOUSE	1	mus musculu
1342	70.5	5.9	662	Q8C6H4	Q8C6H4	2	mus musculu
1343	70.5	5.9	662	Q8C7F9	Q8C7F9	2	mus musculu
1344	70.5	5.9	667	Q9G864	Q9G864	2	malawimonas
1345	70.5	5.9	676	Q7QI4	Q7QI4	2	anopheles g

No.	%1	%2	Len	Accession	ID	N	Organism
1346	70.5	5.9	676	Q7rnv6	Q7RNV6	2	plasmodium
1347	70.5	5.9	679	Q7Q645	Q7Q645	2	anopheles g
1348	70.5	5.9	683	Q972h7	Q972H7	2	sulfolobus
1349	70.5	5.9	689	Q72yu0	Q72YU0	2	bacillus ce
1350	70.5	5.9	700	Q9ldt0	Q9LDTO	2	arabidopsis
1351	70.5	5.9	717	Q6nh18	Q6NHL8	2	corynebacte
1352	70.5	5.9	729	Q8esc5	Q8ESC5	2	oceanobacil
1353	70.5	5.9	740	Q7xcm9	Q7XCM9	2	oryza sativ
1354	70.5	5.9	766	Q9frk0	Q9FRKO	2	oryza sativ
1355	70.5	5.9	766	Q9lz30	Q9LZ30	2	arabidopsis
1356	70.5	5.9	769	Q7w1t5	Q7W1T5	2	bordetella
1357	70.5	5.9	776	P23316	CHS1_CANAL	1	candida alb
1358	70.5	5.9	856	Q9fhv2	Q9FHV2	2	arabidopsis
1359	70.5	5.9	899	Q9ff14	Q9FF14	2	arabidopsis
1360	70.5	5.9	951	Q6fk21	Q6FK21	2	candida gla
1361	70.5	5.9	980	Q8a3j1	Q8A3J1	2	bacteroides
1362	70.5	5.9	1026	Q9urm1	Q9URM1	2	candida alb
1363	70.5	5.9	1199	Q9y4j9	Q9Y4J9	2	homo sapien
1364	70.5	5.9	1234	Q8vd34	Q8VD34	2	mus musculu
1365	70.5	5.9	1234	Q6b4r6	Q6B4R6	2	mus musculu
1366	70.5	5.9	1491	Q7s5p1	Q7S5P1	2	neurospora
1367	70.5	5.9	1583	Q92ge9	Q92GE9	2	rickettsia
1368	70.5	5.9	1678	Q68d82	Q68D82	2	homo sapien
1369	70.5	5.9	1764	Q8mua3	Q8MUA3	2	strongyloce
1370	70.5	5.9	1781	O02952	AK12_HUMAN	1	homo sapien
1371	70.5	5.9	1787	O22516	CHD3_CAEEL	1	caenorhabdi
1372	70.5	5.9	5138	Q9zw94	Q9ZW94	2	arabidopsis
1373	70	5.9	80	Q7n019	Q7N019	2	photorhabdu
1374	70	5.9	114	Q6vrh8	Q6VRH8	2	helicobacte
1375	70	5.9	114	Q75x16	Q75XL6	2	helicobacte
1376	70	5.9	146	Q8t098	Q8T098	2	drosophila
1377	70	5.9	154	O02781	ML1A_PIG	1	sus scrofa
1378	70	5.9	161	Q65j32	Q65J32	2	bacillus li
1379	70	5.9	173	Q67ew5	Q67EW5	2	equine arte
1380	70	5.9	173	Q9wd20	Q9WD20	2	equine arte
1381	70	5.9	173	Q9wd23	Q9WD23	2	equine arte
1382	70	5.9	173	Q9wd35	Q9WD35	2	equine arte
1383	70	5.9	175	Q9hl28	Q9HL28	2	thermoplasm
1384	70	5.9	185	Q81al4	Q8LAL4	2	arabidopsis
1385	70	5.9	189	O49347	PSBY_ARATH	1	arabidopsis
1386	70	5.9	195	Q86fg5	Q86FG5	2	schistosoma
1387	70	5.9	195	Q85qz5	Q85QZ5	2	lepus europ
1388	70	5.9	199	P80470	PSBY_SPIOL	1	spinacia ol
1389	70	5.9	213	Q9lnr6	Q9LNR6	2	arabidopsis
1390	70	5.9	221	Q9b9f3	Q9B9F3	2	viverra zib
1391	70	5.9	223	Q91nk4	Q91NK4	2	avian infec
1392	70	5.9	224	Q8vsw5	Q8VSW5	2	staphylococ
1393	70	5.9	225	Q9j4a6	VME1_IBVD1	1	avian infec
1394	70	5.9	225	Q9j3n8	VME1_IBVDE	1	avian infec
1395	70	5.9	225	Q91gb7	VME1_IBVM	1	avian infec
1396	70	5.9	225	Q6vur1	Q6VUR1	2	avian infec
1397	70	5.9	225	Q6vur2	Q6VUR2	2	avian infec
1398	70	5.9	225	Q6w9d6	Q6W9D6	2	avian infec
1399	70	5.9	236	Q7teh1	Q7TEH1	2	avian infec
1400	70	5.9	238	Q8rie1	Q8RIE1	2	fusobacteri
1401	70	5.9	249	Q9xmr1	Q9XMR1	2	phlebotomus
1402	70	5.9	253	Q6t2a1	Q6T2A1	2	polyrhachis
1403	70	5.9	253	Q7nt81	Q7NT81	2	chromobacte
1404	70	5.9	255	Q995w3	Q995W3	2	equine arte
1405	70	5.9	256	Q9qkf1	Q9QKF1	2	equine arte
1406	70	5.9	256	O76899	O76899	2	drosophila
1407	70	5.9	256	Q65va1	Q65VA1	2	mannheimia
1408	70	5.9	257	Q876g0	Q876G0	2	saccharomyc
1409	70	5.9	281	Q70Q29	Q70Q29	2	necator ame
1410	70	5.9	287	Q9xf88	CB4B_ARATH	1	arabidopsis
1411	70	5.9	289	Q8hzf4	Q8HZF4	2	gorilla gor
1412	70	5.9	289	Q8hzf5	Q8HZF5	2	pan troglod
1413	70	5.9	289	Q7niv8	Q7NIV8	2	gloeobacter
1414	70	5.9	292	P47645	ATP6_MYCGE	1	mycoplasma
1415	70	5.9	292	Q92kz8	Q92KZ8	2	rhizobium m
1416	70	5.9	295	Q65ur1	Q65UR1	2	mannheimia
1417	70	5.9	299	Q6m0q9	Q6M0Q9	2	methanococc
1418	70	5.9	302	Q9m7x8	Q9M7X8	2	arabidopsis

No.			Len	n	Accession	Organism
1419	70	5.9	303	2	Q8KJ79	rhizobium l
1420	70	5.9	305	2	Q87FQ4	vibrio para
1421	70	5.9	307	2	Q97T64	streptococc
1422	70	5.9	307	2	Q8DRJ7	streptococc
1423	70	5.9	308	2	Q6FSR9	candida gla
1424	70	5.9	311	2	Q9JHE2	rattus norv
1425	70	5.9	325	2	Q9G3Z5	lithobius f
1426	70	5.9	328	2	Q8D0N5	yersinia pe
1427	70	5.9	330	2	Q94303	caenorhabdi
1428	70	5.9	332	2	Q85EE3	mitu tubero
1429	70	5.9	333	1	GPR8_HUMAN	homo sapien
1430	70	5.9	333	2	Q6NWQ5	homo sapien
1431	70	5.9	333	2	Q6NWQ6	homo sapien
1432	70	5.9	345	2	Q6X0B5	homo sapien
1433	70	5.9	345	2	Q6X0B8	anolis whit
1434	70	5.9	345	2	Q6X0C1	anolis whit
1435	70	5.9	345	2	Q6X0C4	anolis whit
1436	70	5.9	345	2	Q8TNU4	anolis whit
1437	70	5.9	353	2	Q9XMT1	methanosarc
1438	70	5.9	365	2	Q6A7G0	tetrahymena
1439	70	5.9	369	2	Q9NT82	propionibac
1440	70	5.9	371	2	Q6UVN5	homo sapien
1441	70	5.9	378	2	Q71FH4	loxodonta c
1442	70	5.9	378	2	CYB_SORTU	mungotictis
1443	70	5.9	379	1	CYB_ZIPCA	sorex tundr
1444	70	5.9	379	1	Q47978	ziphius cav
1445	70	5.9	379	2	Q47983	thomomys bo
1446	70	5.9	379	2	Q47994	thomomys bo
1447	70	5.9	379	2	Q8LVE7	thomomys um
1448	70	5.9	379	2	Q8LWD6	proteles cr
1449	70	5.9	379	2	Q8W935	parahyaena
1450	70	5.9	379	2	Q8WDU4	thomomys ma
1451	70	5.9	379	2	Q8WEK4	cratogeomys
1452	70	5.9	379	2	Q34837	thomomys ta
1453	70	5.9	379	2	Q6TL84	kogia simus
1454	70	5.9	379	2	Q71FH8	geomys texe
1455	70	5.9	379	2	Q7Y8J5	nandinia bi
1456	70	5.9	379	2	Q8HB13	procavia ca
1457	70	5.9	379	2	Q8HBC6	thomomys bo
1458	70	5.9	379	2	Q8HBJ3	thomomys bo
1459	70	5.9	379	2	Q8HBK4	thomomys bo
1460	70	5.9	379	2	Q8HHJ3	thomomys bo
1461	70	5.9	379	2	Q8HHJ5	thomomys bo
1462	70	5.9	379	2	Q8HHJ6	thomomys bo
1463	70	5.9	379	2	Q8HHJ8	thomomys bo
1464	70	5.9	380	2	Q6E3J6	thomomys bo
1465	70	5.9	380	2	Q34289	dasyurus al
1466	70	5.9	381	1	CYB_DASAL	dasyurus ha
1467	70	5.9	381	1	CYB_DASHA	dasyurus sp
1468	70	5.9	381	1	CYB_DASSP	dasyurus vi
1469	70	5.9	381	1	CYB_DASVI	myoictis me
1470	70	5.9	381	1	CYB_MYOME	myoictis wa
1471	70	5.9	388	1	CYB_MYOWA	mus musculu
1472	70	5.9	388	1	OXYR_MOUSE	rattus norv
1473	70	5.9	388	1	OXYR_RAT	rattus norv
1474	70	5.9	399	2	Q8R561	homo sapien
1475	70	5.9	399	2	Q96A40	manis tetra
1476	70	5.9	407	2	Q8MID0	streptococc
1477	70	5.9	407	2	086894	streptococc
1478	70	5.9	416	2	Q9RIN7	arabidopsis
1479	70	5.9	418	2	Q9M0N4	legionella
1480	70	5.9	418	2	O54543	legionella
1481	70	5.9	420	2	Q6QFB3	thermotoga
1482	70	5.9	420	2	Q9WZ65	arabidopsis
1483	70	5.9	427	2	082490	parachlamyd
1484	70	5.9	427	2	Q6MDN6	escherichia
1485	70	5.9	437	2	Q8X5S1	escherichia
1486	70	5.9	437	2	Q8FAY1	shigella fl
1487	70	5.9	437	2	Q83P88	agrobacteri
1488	70	5.9	438	2	Q8UJM3	equid herpe
1489	70	5.9	450	2	O39292	plasmodium
1490	70	5.9	452	2	Q7RNL9	photorhabdu
1491	70	5.9	461	2	Q7N4W5	yarrowia li
1492	70	5.9	467	2	Q8MPH2	trypanosoma
1493	70	5.9	476	2	Q6AQF5	desulfotale
1494	70	5.9	479	2	O87T34	vibrio chol
1495	70	5.9	494	2	Q23508	caenorhabdi
1496	70	5.9	494	2	Q8NXW6	staphylococ
1497	70	5.9	494	2	Q99W27	staphylococ
1498	70	5.9	494	2	Q7A762	staphylococ
1499	70	5.9	494	2	Q6GBQ3	staphylococ
1500	70	5.9	494	2	Q6GJ85	staphylococ

ALIGNMENTS

RESULT 1
MENT_HUMAN
```
ID   MENT_HUMAN     STANDARD;      PRT;     234 AA.
AC   O95772;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   MLN64 N-terminal domain homolog (STARD3 N-terminal like protein)
DE   (UNQ855/PRO1864).
GN   Name=STARD3NL; Synonyms=MENTHO;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND
RP   ALTERNATIVE INITIATION.
RC   TISSUE=Fetal brain;
RX   MEDLINE=22384343; PubMed=12393907; DOI=10.1074/jbc.M208290200;
RA   Alpy F., Wendling C., Rio M.-C., Tomasetto C.;
RT   "MENTHO, a MLN64 homologue devoid of the START domain.";
RL   J. Biol. Chem. 277:50780-50787(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P., Gray A.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Arnett C., Wohldmann P., Le T.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, 1 (shown here) and 2, are produced by
CC         alternative initiation;
CC   -!- PTM: Phosphorylated.
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AJ492267; CAD37353.1; -.
DR   EMBL; AY358645; AAQ89008.1; -.
DR   EMBL; AC006033; AAS07552.1; -.
DR   EMBL; BC003074; AAH03074.1; -.
DR   EMBL; BC005959; AAH05959.1; -.
DR   Genew; HGNC:19169; STARD3NL.
KW   Alternative initiation; Phosphorylation; Transmembrane.
FT   CHAIN         1    234       MLN64 N-terminal domain homolog, isoform
FT                                1.
FT   CHAIN         8    234       MLN64 N-terminal domain homolog, isoform
FT                                2.
FT   INIT_MET      8      8       For isoform 2.
FT   DOMAIN       48    218       MENTAL.
FT   DOMAIN        1     53       Cytoplasmic (Potential).
FT   TRANSMEM     54     74       Potential.
FT   DOMAIN       75     97       Extracellular (Potential).
FT   TRANSMEM     98    118       Potential.
FT   DOMAIN      119    122       Cytoplasmic (Potential).
FT   TRANSMEM    123    143       Potential.
FT   DOMAIN      144    150       Extracellular (Potential).
FT   TRANSMEM    151    171       Potential.
FT   DOMAIN      172    234       Cytoplasmic (Potential).
SQ   SEQUENCE   234 AA;  26654 MW;  AFB7DAE381983FB0 CRC64;

Query Match             100.0%;  Score 1195;  DB 1;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 3.3e-100;
Matches  234;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60

Qy    61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRL 120

Qy   121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVYVLPIISFILAWIETWFLDFKVLPQEA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVYVLPIISFILAWIETWFLDFKVLPQEA 180

Qy   181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL 234
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL 234

RESULT 2
MENT_MOUSE
ID   MENT_MOUSE     STANDARD;      PRT;    235 AA.
AC   Q9DCI3; Q99J63; Q9D3S6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DE   05-JUL-2004 (Rel. 44, Last annotation update)
DE   MLN64 N-terminal domain homolog (STARD3 N-terminal like protein).
GN   Name=Stard3nl; Synonyms=Mentho;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Kidney;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume M., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Breast;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Name=1;
CC           IsoId=Q9DCI3-1; Sequence=Displayed;
CC         Name=2;
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```
CC        IsoId=Q9DCI3-2; Sequence=VSP_003909;
CC        Note=No experimental confirmation available;
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- CAUTION: Ref.1 (BAB31166) sequence differs from that shown due to
CC        a frameshift in position 31.
CC   ----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------
DR   EMBL; AK002760; BAB22337.1; -.
DR   EMBL; AK018331; BAB31166.1; ALT_FRAME.
DR   EMBL; BC003334; AAH03334.1; -.
DR   MGD; MGI:1923455; Stard3nl.
KW   Alternative splicing; Transmembrane.
FT   DOMAIN       48    218       MENTAL.
FT   DOMAIN        1     53       Cytoplasmic (Potential).
FT   TRANSMEM     54     74       Potential.
FT   DOMAIN       75     97       Extracellular (Potential).
FT   TRANSMEM     98    118       Potential.
FT   DOMAIN      119    122       Cytoplasmic (Potential).
FT   DOMAIN      123    143       Potential.
FT   TRANSMEM    144    150       Extracellular (Potential).
FT   DOMAIN      151    171       Potential.
FT   DOMAIN      172    235       Cytoplasmic (Potential).
FT   VARSPLIC    218    235       SEERAEEKQESEKPLLEL -> RNSSAFRMGIQKSSQPSGG
FT                                AAGTRARFVPKASSCREGRPGLPMWLQ (in isoform
FT                                2).
FT                                /FTId=VSP_003909.
FT   CONFLICT     32     33       QL -> HS (in Ref. 1; BAB22337).
FT   CONFLICT     52     52       R -> G (in Ref. 2).
SQ   SEQUENCE    235 AA;  26811 MW;  F251725390CB1503 CRC64;

Query Match             94.9%;  Score 1134.5;  DB 1;  Length 235;
Best Local Similarity   94.9%;  Pred. No. 1e-94;
Matches   223;  Conservative   5;  Mismatches   6;  Indels   1;  Gaps   1;

Qy    1  MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
         |||||:|:||||||||||||||||:||||||:|||||||||||||||||||||||||||
Db    1  MNHLPEHMENTLTGSQSSHASLRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLFVT  60

Qy   61  FDLLFVTILMWIIELNVNGGIENTLKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRL  120
         ||||||||||||||||||||||||||:|||||||||||||||||||||||||:||||||
Db   61  FDLLFVTILMWIIELNVNGGIENTLKKEVIHYDYYSSYFDIFLLAVFRFKVLILGYAVCRL  120

Qy  121  RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA  180

Qy  181  EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGS-EEAEEKQDSEKPLLEL  234
         |||||||||||||||||||||:|||||||||||||||| ::||||||:||||||
Db  181  EEENRLLIVQDASERAALIPAGLSDGQFYSPPESEAGSEEEAEEKQBSEKPLLEL  235

RESULT 3
Q6DI38
ID   Q6DI38         PRELIMINARY;    PRT;   227 AA.
AC   Q6DI38;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Zgc:86628.
GN   Name=zgc:86628;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
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```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Strausberg R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC075752; AAH75752.1; -.
SQ   SEQUENCE    227 AA;  25485 MW;  24C46AD8FF4985C6 CRC64;

Query Match             66.6%;  Score 796;  DB 2;  Length 227;
Best Local Similarity   68.3%;  Pred. No. 5.1e-64;
Matches   155;  Conservative   31;  Mismatches   39;  Indels   2;  Gaps   2;

Qy    8  MENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLFVT  67
         |::.||| |:|:  :||:|||:  ||:|::||.||||||||||||||||||||||||||
Db    1  MDSQCSSSVGSRANLGGLGNINSTPISARVBSYEAGEKKGISDVRRTFCLFVTFDLLFVT  60

Qy   68  LLWIIELNVNGGIENTLKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIA  127
         |||||||||||||:|| :|::||:.||: |||||::|| ||:|||||||||::||||||
Db   61  LLWIIELNVNGGIQQLEQEVLKYDYHKSFFDIFLLAVFRFAALILAYAVCKLRHWWAIA  120

Qy  128  LTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAEEENRLL  187
         :|||| ||||: :::||||||||||||||||||||||||||:|||||||||: :|||:||
Db  121  ITTAITTGFLVKVVVSKLLSQGAFGYVLPIISFILAWIETWLLDFKVLPQEAGDEIRYL  180

Qy  188  IVQDASERAALI-PGGLSDGQFYSPPESEAGS-ERAEEKQDSEKPLL  232
         :|:|  :|: || ::| |:|||||:||||| : :::|||| ||||:|
Db  181  SVQNRLEHEPLLPPGPLSEGLFYSPPESLADSDEDLDDKHDLEKPIV  227

RESULT 4
Q6DFR7
ID   Q6DFR7         PRELIMINARY;    PRT;   448 AA.
AC   Q6DFR7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Stard3-prov protein.
GN   Name=stard3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
```

RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC076666; AAH76666.1; -.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE 448 AA; 50926 MW; 2686D07C737D4204 CRC64;

Query Match   58.6%; Score 700.5; DB 2; Length 448;
  Best Local Similarity 61.1%; Pred. No. 5.2e-55;
  Matches 143; Conservative   29; Mismatches   49; Indels   13; Gaps   4;

Qy   1 MNHLP---EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC 56
          |||| |:| :|: || |:| ::: |||||||
Db   1 MTKLPGDFQPDLERSLPAIASINSSMSQNHVFSPHSLLPR------EQRRVISDVRRTFC 54

Qy   57 LFVTFDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVPRFKVLILAYA 116
          ||||||||:||:||||||||| :|||:||:||||||||||||| |: :||||||||
Db   55 LFVTFDLLFISLLMWIIELNTNDGIEKNLEEILHYDFKNSFFDIFLLAVPRFSVLILAYA 114

Qy 117 VCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL 176
          |:|||||||||:|: |||||||:||:|:||||:|||||:||:|||:||||||:||||||
Db 115 IVRLRHWWAIAITTLVTSAFLIAKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL 174

Qy 177 PQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEEAEEKQDSEK 229
          |||: |||| |:: ||| |: ||||||||||||||||||: |: :||
Db 175 TQEAEERWYMAVQAAGSHPPLLYNGALSDGQFYSPPESFAGSD--NEFDDDEE 226

RESULT 5
Q6PF40
ID   Q6PF40   PRELIMINARY;   PRT;   444 AA.
AC   Q6PF40;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC68989 protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC057738; AAH57738.1; -.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;

Query Match   58.5%; Score 698.5; DB 2; Length 444;
  Best Local Similarity 60.9%; Pred. No. 7.9e-55;
  Matches 140; Conservative   30; Mismatches   51; Indels   9; Gaps   3;

Qy   1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
Db   1 MTKIPGDFQPDLERSLPAIASMSQSHVFSPRSLLPR------EQRRAISDVRRTFCLFVT 54

Qy   61 FDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVPRFKVLILAYAVCRL 120
Db   55 FDLLFISLLMWIIELNTNNGIEKNLEEILYDFKNSFFDIFLLAVPRFSVLILAYAIVRL 114

Qy 121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
Db 115 RHWWAIAITTLVTSAFLIVKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLTQEA 174

Qy 181 EEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEEAEEKQDSEK 229
Db 175 EEERWYIAAQAAATHPSLLYNGALSDGQFYSPPESFAGSD--NEFDDEEE 222

RESULT 6
Q6GNT3
ID   Q6GNT3   PRELIMINARY;   PRT;   448 AA.
AC   Q6GNT3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC80895 protein.
GN   Name=MGC80895;

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OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OX   Xenopodinae; Xenopus.
     NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073419; AAH73419.1; -.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE   448 AA;  51279 MW;  472FF8E7C3B2F5E4 CRC64;

Query Match             57.2%;  Score 684;  DB 2;  Length 448;
Best Local Similarity   59.7%;  Pred. No. 1.6e-53;
Matches 139;  Conservative 34;  Mismatches 48;  Indels 12;  Gaps 4;

Qy          1 MNHLP---EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC 56
              ||:||   | :|   | |:| |  :| : :|:|  |    : | |:    |::|||||||
Db          1 MTKLPGEFQPDLERSLPAIASINSSMSHNHVFSPHSLLPR------BQRRLISDVRRTFC 54

Qy         57 LFVTFDLLFVTLMWIIELNVNGGIENTLEKEVMQYDYSSYDIFLLAVFRFKVLILAYA 116
              |||||||||||:::||||||||| ||| :|:||  |:||||::||||||||||||||||
Db         55 LFVTFDLLFISLLMWIIBLNTNNGIEKNLBEEILHYDFKNSFFDIYLLAVFRFSVLILAYA 114

Qy        117 VCRLRHWHAIALTTAVTSAFLLAKVILSKLFSQGAFGVYLPIISFILAWIETWFLDFKVL 176
              ||| |::|| |  | |||||| | : |:| || |||| ||||:|| ||||:|||||||||
Db        115 IVRLRHWHAIAITTLVTSAFLIVKVIQSGLLSKGAFGVYLPIVSFVLAWLETWFLDFKVL 174

Qy        177 PQEAEENRLLIVQ-DASERAALIPGGLSDGQFYSPPESEAGSE-EABEKQDS 227
              || ||| | | |   |    |  ||| |  ||||||||::||  |:|:::|::
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     Db   175 TQEAEERWYTAAQAPANHPPYLYNGTLSDGQYSPPESPAGSDNEFEDEEEA 227

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RESULT 7
ML64_HUMAN
ID   ML64_HUMAN   STANDARD;   PRT;   445 AA.
AC   Q14849; Q96HM9;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   MLN 64 protein (StAR-related lipid transfer protein 3) (StARD3) (START
DE   domain-containing protein 3) (CAB1 protein).
GN   Name=STARD3; Synonyms=CAB1, MLN64;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast carcinoma;
RX   MEDLINE=9603945; PubMed=7490069;
RA   Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA   Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT   "Identification of four novel human genes amplified and overexpressed
RT   in breast carcinoma and localized to the q11-q21.3 region of
RT   chromosome 17.";
RL   Genomics 28:367-376(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Oesophageal carcinoma;
RX   MEDLINE=97413641; PubMed=9270027;
RA   Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M.,
RA   Hirai H., Yazaki Y., Sugimura T., Terada M.;
RT   "Isolation of a candidate gene, CAB1, for cholesterol transport to
RT   mitochondria from the c-ERBB-2 amplicon by a modified cDNA selection
RT   method.";
RL   Cancer Res. 57:3548-3553(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung, Skin, and Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445.
RX   MEDLINE=20264523; PubMed=10802740; DOI=10.1038/75192;
RA   Tsujishita Y., Hurley J.H.;
RT   "Structure and lipid transport mechanism of a StAR-related domain.";
RL   Nat. Struct. Biol. 7:408-414(2000).
RN   [5]
RP   TOPOLOGY.
RX   MEDLINE=21264925; PubMed=11053434; DOI=10.1074/jbc.M006279200;
RA   Alpy F., Stoeckel M.-E., Dierich A., Escola J.-M., Wendling C.,
RA   Chenard M.-P., Vanier M.T., Gruenberg J., Tomasetto C., Rio M.-C.;
RT   "The steroidogenic acute regulatory protein homolog MLN64, a late
```

```
RT   endosomal cholesterol-binding protein.";
RL   J. Biol. Chem. 276:4261-4269(2001).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis in placenta and brain.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein.
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- SIMILARITY: Contains 1 START domain.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/MLN64ID202.html".
```
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DR   EMBL; X80198; CAA56489.1; -.
DR   EMBL; D38255; BAA22525.1; -.
DR   EMBL; BC008356; AAH08356.1; -.
DR   EMBL; BC008747; AAH08747.1; -.
DR   EMBL; BC025679; AAH25679.1; -.
DR   PIR; I38027; I38027.
DR   PDB; 1EM2; X-ray; A=216-444.
DR   Genew; HGNC:17579; STARD3.
DR   H-InvDB; HIX0013780; -.
DR   MIM; 607048; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0008203; P:cholesterol metabolism; TAS.
DR   GO; GO:0006839; P:mitochondrial transport; TAS.
DR   GO; GO:0008202; P:steroid metabolism; TAS.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   3D-structure; Lipid transport; Lipid-binding; Steroidogenesis;
KW   Transmembrane; Transport.
FT   DOMAIN        1     51       Cytoplasmic (Potential).
FT   TRANSMEM     52     72       Potential.
FT   DOMAIN       73     94       Extracellular (Potential).
FT   TRANSMEM     95    115       Potential.
FT   DOMAIN      116    120       Cytoplasmic (Potential).
FT   TRANSMEM    121    141       Potential.
FT   DOMAIN      142    148       Extracellular (Potential).
FT   TRANSMEM    149    169       Potential.
FT   DOMAIN      170    445       Cytoplasmic (Potential).
FT   DOMAIN       46    217       MENTAL.
FT   DOMAIN      230    443       START.
FT   CONFLICT    117    117       Q -> R (in Ref. 3; AAH08356/AAH25679).
FT   CONFLICT    216    216       G -> A (in Ref. 3; AAH25679).
FT   HELIX       233    253
FT   TURN        254    255
FT   HELIX       256    258
FT   STRAND      260    264
FT   TURN        266    267
FT   STRAND      270    276
FT   TURN        277    279
FT   STRAND      280    289
FT   HELIX       293    299
FT   TURN        300    302
FT   HELIX       304    307
FT   TURN        308    310
FT   TURN        312    313
FT   STRAND      314    323
FT   TURN        324    326
FT   STRAND      327    334
FT   STRAND      337    337
FT   TURN        338    341
FT   STRAND      342    342
FT   STRAND      345    355
FT   STRAND      359    366
FT   TURN        370    371
FT   TURN        376    377
FT   STRAND      379    380
FT   STRAND      382    383
FT   STRAND      386    392
FT   TURN        397    398
FT   STRAND      400    406
FT   STRAND      408    409
FT   HELIX       416    440
FT   TURN        441    442
SQ   SEQUENCE   445 AA;  50474 MW;  62BD5C3EDA0DDEF CRC64;

Query Match             55.6%;  Score 664;  DB 1;  Length 445;
Best Local Similarity   56.2%;  Pred. No. 1.1e-51;
Matches  135;  Conservative  38;  Mismatches  45;  Indels  22;  Gaps   5;

Qy     1 MNHLP----EDMENAL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
          |:|       :|:|            |:: :||:|  :||        ::: ||||
Db     1 MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHLLPPB----------KRRAISDV 49

Qy    52 RRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVL 111
          ||||||||||||||||||||||||||  |:|:||||:|||||:||:|  |||||
Db    50 RRTFCLFVTFDLLFISLLWIIELNTNTGIRKNLEQEIIQXNFKTSPFDIFVLAFPRFSGL 109

Qy   112 ILAYAVCRLRHWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
          :|| | ::|| |::  :|: ||:||  |||::|||  :|||||  ||||:|||:|||
Db   110 LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL 169

Qy   172 DFKVLPQEABEBNRLLIVQDASERAALI-PGGLSDQFYSPPESEAGSE-EABEKQDSEK 229
          ||||||||||| |:: :|||||:|:|::||        ::|::|:: :|:|:
Db   170 DFKVLPQEABEBRWYLAAQVAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEBVAGKK 229

RESULT 8
ML64_MOUSE
ID   ML64_MOUSE     STANDARD;      PRT;    446 AA.
AC   Q61542;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   MLN 64 protein (StAR-related lipid transfer protein 3) (StARD3) (START
DE   domain-containing protein 3) (ES 64 protein).
GN   Name=Stard3; Synonyms=Es864, Mln64;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96039245; PubMed=7490069;
RA   Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA   Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT   "Identification of four novel human genes amplified and overexpressed
RT   in breast carcinoma and localized to the q11-q21.3 region of
RT   chromosome 17.";
RL   Genomics 28:367-376(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis in placenta and brain (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein (By similarity).
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- SIMILARITY: Contains 1 START domain.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; X82457; CAA57834.1; -.
DR   EMBL; BC003313; AAH03313.1; -.
DR   HSSP; Q14849; 1EM2.
DR   MGD; MGI:1929618; Stard3.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Lipid transport; Lipid-binding; Steroidogenesis; Transmembrane;
KW   Transport.
FT   DOMAIN        1     52       Cytoplasmic (Potential).
FT   TRANSMEM     53     73       Potential.
FT   DOMAIN       74     95       Extracellular (Potential).
FT   TRANSMEM     96    116       Potential.
FT   DOMAIN      117    121       Cytoplasmic (Potential).
FT   TRANSMEM    122    142       Potential.
FT   DOMAIN      143    149       Extracellular (Potential).
FT   TRANSMEM    150    170       Potential.
FT   DOMAIN      171    446       Cytoplasmic (Potential).
FT   DOMAIN       47    218       MENTAL.
FT   DOMAIN      231    444       START.
SQ   SEQUENCE   446 AA;  50469 MW;  DBF435S604F3B1E2 CRC64;
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Query Match 54.9%; Score 656.5; DB 1; Length 446;
Best Local Similarity 57.8%; Pred. No. 5.1e-51;
Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;

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Qy      7 DMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTF 61
            |:|  :|    |||::||   : |   |                   ::: |||||||||
Db     11 DLERSLPALASLGTSLSHSQSLSSHFIPPPL-------EKRRAISDVRRTFCLFVTF 60

Qy     62 DLLFVTLLWIIELNVNGGIENTLEKEVMQDYYSSYFDIFLLAVFRFKVLILAYAVCRLR 121
            |||:||||:|||||||||||||||||||||||||:|:|| ||| |:: ||| :||||
Db     61 DLLFISLLWIIELNTNTGIRKNLEQEVIHYSFQSSFFDIPVLAFFRFSGLLLGYAVLRLQ 120

Qy    122 HWAIALTTAVTSAFLLAKVILSKLFSQGAFGVYLPIISFILAWIETWFLDPKVLPQRAE 181
            ||:|||||||||||||||| ||||:||||||||||||||:||||:||||||||||:|||
Db    121 HWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSPVLAWLETWFLDPKVLPQEAE 180

Qy    182 EENRLLIVQDASBRAALi-PGGLSDGQFYSPPESEAGSB-EABEKQDSEK 229
            ||||||| | |:|||||: |||||||||||||||||||| :||:|::| |
Db    181 EERRYLAAQAAVARGPLLFSGALSBGQFYSPPESPAGSDNESDEEVTGKK 230
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AC   Q6PH03;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   START domain containing 3.
GN   Name=stard3;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AB; TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AB; TISSUE=Whole body;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056766; AAH56766.1; -.
DR   ZFIN; ZDB-GENE-001120-2; stard3.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE   448 AA;  50751 MW;  716A18C127B59C5D CRC64;
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Query Match 52.9%; Score 632; DB 2; Length 448;
Best Local Similarity 70.9%; Pred. No. 8.6e-49;
Matches 127; Conservative 18; Mismatches 32; Indels 2; Gaps 2;

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Qy     44 EKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQDYYSSYFDIFLL 103
            |:| |||||||||||||||:|||| :||||||||||||||||::| |:||||||||||
Db     43 ERKAFSDVRRTFCLFVTFDLLFISLLWIIELNISKSIWNSLENEVVHYNFKSSFFDIFLL 102

Qy    104 AVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVYLPIISFIL 163
            |:||| |:: ||| :||| ||  |||||||||||||||||:||||:||||||||||||:|
Db    103 AVFRFLCLQLGYAAFRLRHWVIAITTLVTTAFLIAKVILSDLFSQNAFGVYLPITSFVV 162

Qy    164 AWIETWFLDPKVLPQRABEEN-RLLIVQDASBRAALi-PGGLSDGQFYSPPESEAGSBE 220
            |||||||||||||:| ||| | |||   |||  ||: |||||||||||||||||| ||:
Db    163 AWLETWFLDPKVLTQBAEDERVYLAAVNAACEPAPLICPRPVSDGQFYSPPESLAGSED 221
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AC   Q8BMP8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE   enriched library, clone:5330402M06 product:H_NH1021A08.1 PROTEIN
DE   (UNKNOWN) (PROTEIN FOR MGC:14607) (SIMILAR TO STEROIDOGENIC ACUTE
DE   REGULATORY PROTEIN RELATED) homolog.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue S., Togawa Y., Izawa M., Ohara B., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka K., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato M., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda T., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK030365; BAC26922.1; -.
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SQ   SEQUENCE   107 AA;  12417 MW;  1B30DA6C81465089 CRC64;

     Query Match             41.2%;
     Best Local Similarity   92.2%;    Score 492;  DB 2;  Length 107;
     Matches   94;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
           ||||||:|||.|||||||||||||:||||||.|||||||||||||||||||||||||||
Db     1 MNHLPEHMENVLTGSQSSHASLRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLFVT 60

Qy    61 FDLLFVTLLWIIELNVNGGIENTLKEVMQYDYSSYPDIFL 102
           |||||||||||||||||||||||::||:|||||||||||:
Db    61 FDLLFVTLLWIIELNVNGGIENTLKKVIHYDYSSYPDIFV 102

RESULT 11
Q7QIT3
ID   Q7QIT3             PRELIMINARY;       PRT;    568 AA.
AC   Q7QIT3;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AGCP2158 (Fragment).
GN   Name=agCG52468; ORFNames=ENSANGG00000018959;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008807; EAA03945.1; -.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   PRINTS; PR00978; STARPROTEIN.
DR   PROSITE; PS50848; START; 1.
FT   NON_TER       1      1
FT   NON_TER     568    568
SQ   SEQUENCE   568 AA;  62932 MW;  BCEB3D361A05DF15 CRC64;

     Query Match             29.1%;
     Best Local Similarity   36.6%;    Score 348;  DB 2;  Length 568;
     Matches   86;  Conservative   45;  Mismatches   72;  Indels   32;  Gaps    9;

Qy    13 TGSQSSHASLRNIHSINPTQLMAR--IESYEGREKKGISDVRRTFCLFVTFDLLFVTLLW 70
          |||| ||| ||:|  |  |:  | |:    : |:|||||||||||||||||||:|||||||
Db     1 TRSQS------HTVN--LLSEDFIAGY-MEQGRMSVVRRFFCLFVTFDVVFISLLW 47

Qy    71 IIELNVNG-GIENTLKEVMQYDYSSYFDIFLLAVFRFKVLLLAYAVCRLRHWWAIALT 129
          ||||||||:||||| ::| |:|||:|  :| ||:::||:|||:||||||||||||||:
Db    48 IICVITGDNVIHALQTQVLHYTVYTSLFDVVIAALIRFIFLILFYGLLSISHWLVIAlS 107

Qy   130 TAVTSAFLLAKVILSKLFS--QGAFGVVLPIISFLLAWIETWFLDFKVLPQEABENRLL 187
          ||:||||| |:|| ||:||    :|| |:| : |:|||| |:|||||::|| :|: :
Db   108 TTSSCAFLISKVFLYDWTATPQPVFEVLLIVVSFVLAWGEAWFLDCRVIPQBRYARNYFV 167

Qy   188 IVQDASERAALIP----------GGLSD--GQFYSPPES--EAGSEEAEEKQDSE 228
           :  : ||||| |         ::|||  ||: ||| ::  :|:||| |: :||
Db   168 AITNPGSMDARTPLLDPFLSAMQAGRTESIGNFYSPFDSIHNSDDDDBDEQDDE 222

RESULT 12
Q8MZH4
ID   Q8MZH4             PRELIMINARY;       PRT;    545 AA.
AC   Q8MZH4;
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DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DB   LD23890p (CG3522-PB).
GN   ORFNames=CG3522;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorset V., Dreenek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhu H.O.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Wan K.H., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.B., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102683; AAM27512.1; -.
DR   EMBL; AE003464; AAS64770.1; -.
DR   FlyBase; FBgn0035028; CG3522.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   PRINTS; PR00978; STARPROTEIN.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE 545 AA; 61429 MW; 5F6RAF98AC917160 CRC64;

Query Match   28.7%; Score 343; DB 2; Length 545;
Best Local Similarity 37.8%; Pred. No. 1.8e-22;
Matches 90; Conservative 44; Mismatches 76; Indels 28; Gaps 10;

Qy   8 MENALTGSQSSHA--SLRNIHSINPTQLMARIESYEGREKKG-ISDVRRTFCLFVTFDLL 64
            |||:.||:| ||||||| | |||||||||||||||||||
Db   17 LANARQGNSAYNMQYDMSRAHSIN---LITEDFLAGYMQDGRMSVVRRFFCLFVTFDLV 72

Qy   65 FVTLLWIIELNVNG-GIENTLEKEWMQYDVYSSYFDIFLLAVFRFKVLILAYAVCRLRHW 123
           ||:||:| |||::|| |::.|| ||| :||: ||||||||:|
Db   73 FVSLLWLICIVINGDNIFTAFHKQIVEYTIYKSLFDVVAVAICRFLVLIFFYAILYINHW 132

Qy   124 WAIALTTAVTSAFLLAKVIL----SKLFSQGAFGVVLPIISFILAWIETWFLDFKVLPQ 178
           |||:|.|:| ||||| | :||:| |||||||||||||||| |:.|:|
Db   133 SIIALSTSGGSCLFLISKVFVFDWLDSK--QQVFEVILITSFILAWGEAWFLDCRVIPQ 189

Qy   179 E-ABEENRLLIVQDAS--ERAALI------PGGLSDGQFYSPPESAGSEEABEKQD 226
           : :.:| |:||| ||: ||: |||:
Db   190 ERHAQHYFRTMTSNDRTPMEQPAILIEQERPQSVTD--FYSLMDTARHSDEDBLDD 245

RESULT 13
Q9W145
ID   Q9W145   PRELIMINARY;   PRT;   583 AA.
AC   Q9W145;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   CG3522-PA (Putative cholesterol transporter).
GN   ORFNames=CG3522;
OS   Drosophila melanogaster (Fruit fly).

OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RX   PubMed=14745013; DOI=10.1073/pnas.0308212100;
RA   Roth G.E., Gierl M.S., Vollborn L., Meise M., Lintermann R., Korge G.;
RT   "The Drosophila gene Start1: a putative cholesterol transporter and
RT   key regulator of ecdysteroid synthesis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:1601-1606(2004).
DR   EMBL; AE003464; AAF47232.2; -.
DR   EMBL; AY455866; AAR19767.1; -.
DR   IntAct; Q9W145; -.
DR   FlyBase; FBgn0035028; CG3522.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 2.
DR   PRINTS; PR00978; STARPROTEIN.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE 583 AA; 65822 MW; F043047A5ADD6FF1 CRC64;

Query Match   28.7%; Score 343; DB 2; Length 583;
Best Local Similarity   37.8%; Pred. No. 2e-22;
Matches   90; Conservative 44; Mismatches 76; Indels 28; Gaps 10;

Qy   8 MENALTGSQSHA--SLRNIHSINPTQLMARIESYEGREKKG-ISDVRRTFCLFVTFDLL 64
            |||||||| |||| ||||||||||| |||||||||||
Db   17 LANARQGNSAYNMQYDMSRAHSIN---LITEDFLAGYMQDGRMSVVRRFPCLFVTFDLV 72

Qy   65 FVTLLWIIELNVNG-GIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHW 123
            ||||||||| :||| |||||: |:||| |||| :|:| |||| :||:|
Db   73 FVSLLWLICIVINGDNIFTAPHKQIVEYTIYKSLPDVVAVICRFLVLIFPFYAILYINHW 132

Qy 124 WAIALTTAVTSAFLLAKVIL----SKLFSQGAFGVVLPIISFILAWIETWFLDFKVLPQ 178
            |||:||||| || ||:|| ||:||:||
Db 133 SIIALSTSGSCLFLISKVFVFDWLDSK---QQVFEVILITSFILAWGEAWFLDCRVIPQ 189

Qy 179 E--AEEENRLLIVQDAS--ERAALI-----PGGLSDGQFYSPPESEAGSEAEEKQD 226
             |:|| :| ||:: |:| ||:|
Db 190 ERHAQHYFRTMTSNDRTPMEQPAILIEQERPPQSVTD--FYSLMDTARHSDEDELDD 245

RESULT 14
Q19819
ID   Q19819   PRELIMINARY;   PRT;   447 AA.
AC   Q19819;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein F26F4.4.
GN   ORFNames=F26F4.4, F26F4.4;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;

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RG   WormBase Consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Fulton L.;
RT   "The sequence of C. elegans cosmid F26F4.";
RL   Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Wilson R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RG   WormBase Consortium;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U12964; AAA91219.3; -.
DR   PIR; T16170; T16170.
DR   WormBase; WBGene00017826; F26F4.4.
DR   WormPep; F26F4.4; CE30767.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   447 AA;  51543 MW;  D86394844670113 CRC64;

Query Match             17.1%;  Score 204; DB 2; Length 447;
Best Local Similarity   26.5%;  Pred. No. 5.9e-10;
Matches   56;  Conservative   36;  Mismatches   73;  Indels   46;  Gaps    6;

Qy    42 GREKKGISDVRRTFCLFVTFDLLFVTLMII----------------ELNVNGGIENTLEK 86
             : ::|:|:|: |.:::|: :|||::
Db    11 GSQRIGVSKDRKRFIVITFPDTSITILLMLLCTVTRDDDWDKVFNEINI---------FNP 63

Qy    87 EVMQYDYYSSYFDIFLLAVFRFKVLLAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKL 146
             : ::     |||| ||||| ||: |. ||: |: :|:|||::|||:|
Db    64 KFIRI----SLFDIVLLAVLRMLLGVVVGICLVKQWYTVAFTTLASSAYILMKVLFYFN 119

Qy   147 FSQGAFGYVLPII-SFILAWIETWFLDFKFKVLPQEABEENRLLIVQDASERAALIPGGLSD 205
             : :|||:||:|:: |:||:|: |:::|:|:|  |  | :|:||||
Db   120 HSSSAVPPLLLIITSFTLCWSEFYLMPFQILPRERRYARREL-----------DGIEN 166

Qy   206 GQFYSPPPESEA------GSBEAEBKQDSEKP 230
             :|::|||::|:        | |
Db   167 PEFSTDDEARSNNRHRRGRRQQNSGNQSEAP 197
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RESULT 15
ML64_SALFO
ID   ML64_SALFO      STANDARD;      PRT;     294 AA.
AC   Q9OZB9;
DT   28-FEB-2003  (Rel. 41, Created)
DT   28-FEB-2003  (Rel. 41, Last sequence update)
DT   05-JUL-2004  (Rel. 44, Last annotation update)
DE   MLN64-like protein (Fragment).
GN   Name=MLN64;
OS   Salvelinus fontinalis (Brook trout) (Brook char).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX   NCBI_TaxID=8038;
RN   [1]
RP   SEQUENCE FROM N.A.
```

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RA   Goetz F.W.;
RT   "Cloning and characterization of trout MLN64.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binds and transports cholesterol. Promotes
    steroidogenesis (By similarity).
-!- SIMILARITY: Contains 1 START domain.
```

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DR   EMBL; AF284379; AAK82981.1; -.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Lipid transport; Lipid-binding; Steroidogenesis; Transport.
FT   NON_TER       1      1
FT   DOMAIN       79    292       START.
SQ   SEQUENCE   294 AA;  32807 MW;  E1C3F2CB32C2BA91 CRC64;

Query Match             8.7%;  Score 104.5; DB 1; Length 294;
Best Local Similarity   66.7%;  Pred. No. 0.39;
Matches   24;  Conservative    3;  Mismatches    8;  Indels    1;  Gaps    1;

Qy   186 LLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEE 220
             |||||||||||| |||:|:||||||:|||||||
Db    33 LAAVNAASERAPMIYPRAVSEGQFYSPPESLAGSEE 68
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Search completed: November 16, 2005, 21:37:43
Job time : 107 secs
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OM protein - protein search, using sw model

Run on: November 16, 2005, 21:28:21 ; Search time 23 Seconds
                                 (without alignments)
                                 759.473 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSQSSHA.........EAGSEAEEKQDSEKPLLEL 234

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   Issued Patents AA:*
           1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
           2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
           3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
           4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
           5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	664	55.6	445	2	US-08-691-814B-6	Sequence 6, Appli
2	85.5	7.2	449	2	US-09-949-016-8594	Sequence 8594, Ap
3	82.5	6.9	341	2	US-08-846-762-92	Sequence 92, Appl
4	80.5	6.7	350	4	US-09-489-039A-9711	Sequence 9711, Ap
5	79.5	6.7	406	4	US-09-171-699-4	Sequence 4, Appli
6	79.5	6.7	406	5	PCT-US94-02107-2	Sequence 2, Appli
7	79.5	6.6	723	4	US-09-976-594-503	Sequence 503, App
8	78.5	6.6	221	4	US-09-270-767-41033	Sequence 41033, A
9	78.5	6.6	221	4	US-09-270-767-56249	Sequence 56249, A
10	78.5	6.6	766	4	US-09-724-653-2	Sequence 2, Appli
11	78.5	6.6	766	4	US-09-724-653-14	Sequence 14, Appl
12	78.5	6.6	766	4	US-09-724-653-15	Sequence 15, Appl
13	78	6.5	228	4	US-09-248-796A-20444	Sequence 20444, A
14	78	6.5	251	4	US-09-270-767-43373	Sequence 43373, A
15	78	6.5	355	4	US-08-833-752-9	Sequence 9, Appli
16	78	6.5	355	4	US-09-938-719-9	Sequence 9, Appli
17	78	6.5	355	4	US-09-939-226B-9	Sequence 2, Appli
18	77	6.4	353	2	US-08-466-103A-14	Sequence 14, Appl
19	77	6.4	353	3	US-09-280-420-2	Sequence 2, Appli
20	77	6.4	353	3	US-09-479-195-2	Sequence 2, Appli
21	76.5	6.4	435	4	US-09-489-039A-12344	Sequence 12344, A
22	76.5	6.4	494	4	US-08-464-340A-4	Sequence 4, Appli
23	76.5	6.4	494	5	PCT-US94-08449A-4	Sequence 4, Appli
24	76	6.4	195	4	US-09-134-000C-5992	Sequence 5992, Ap
25	76	6.4	593	4	US-09-720-317A-22	Sequence 22, Appl
26	75.5	6.3	263	4	US-09-583-110-3148	Sequence 3148, Ap
27	75.5	6.3	264	4	US-09-107-433-4877	Sequence 4877, Ap
28	75.5	6.3	352	4	US-09-492-709A-293	Sequence 293, App
29	75.5	6.3	355	4	US-09-248-796A-14258	Sequence 14258, A
30	75.5	6.3	397	4	US-09-721-870-105	Sequence 105, App
31	75.5	6.3	433	4	US-09-721-870-107	Sequence 107, App
32	75.5	6.3	471	2	US-08-477-451-20	Sequence 20, Appl
33	75.5	6.3	499	4	US-09-721-870-40	Sequence 40, Appl
34	75	6.3	467	4	US-09-328-352-5465	Sequence 5465, Ap
35	75	6.3	549	1	US-09-134-000C-4375	Sequence 4375, Ap
36	74.5	6.3	355	1	US-08-153-848-28	Sequence 28, Appl
37	74.5	6.3	355	4	US-08-153-848-32	Sequence 32, Appl
38	74.5	6.2	355	3	US-09-299-843A-28	Sequence 28, Appl
39	74.5	6.2	355	3	US-09-299-843A-32	Sequence 32, Appl
40	74.5	6.2	355	3	US-09-088-337B-28	Sequence 28, Appl
41	74.5	6.2	355	3	US-09-088-337B-32	Sequence 32, Appl
42	74.5	6.2	355	4	US-09-170-496D-130	Sequence 130, App
43	74.5	6.2	355	4	US-09-170-496D-232	Sequence 232, App
44	74.5	6.2	355	4	US-09-917-254-68	Sequence 68, Appl
45	74.5	6.2	355	5	PCT-US93-11153-28	Sequence 28, Appl
46	74.5	6.2	355	5	PCT-US93-11153-32	Sequence 32, Appl
47	74.5	6.2	471	1	US-07-996-772A-11	Sequence 11, Appl
48	74.5	6.2	471	3	US-09-032-742-2	Sequence 2, Appli
49	74.5	6.2	471	3	US-09-032-742-11	Sequence 11, Appl
50	74.5	6.2	471	3	US-09-032-742-14	Sequence 14, Appl
51	74.5	6.2	471	3	US-09-032-742-17	Sequence 17, Appl
52	74.5	6.2	471	4	US-09-145-864-4	Sequence 4, Appli
53	74.5	6.2	940	4	US-09-328-352-8165	Sequence 8165, Ap
54	74	6.2	154	4	US-09-543-681A-7579	Sequence 7579, Ap
55	74	6.2	332	4	US-09-107-433-2662	Sequence 2662, Ap
56	74	6.2	350	2	US-08-466-103A-12	Sequence 12, Appl
57	74	6.2	353	4	US-08-896-365-6	Sequence 6, Appli
58	74	6.2	680	4	US-09-248-796A-15089	Sequence 15089, A
59	73.5	6.2	312	4	US-09-543-681A-6267	Sequence 6267, Ap
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64	73	6.1	364	4	US-09-077-675A-16	Sequence 16, Appl
65	73	6.1	364	4	US-09-077-674-16	Sequence 16, Appl
66	73	6.1	364	4	US-09-762-661A-6	Sequence 6, Appli
67	73	6.1	364	4	US-09-743-475-3	Sequence 3, Appli
68	73	6.1	364	4	US-09-743-475-5	Sequence 5, Appli
69	73	6.1	377	3	US-08-936-165A-533	Sequence 533, App
70	73	6.1	494	4	US-09-949-016-7475	Sequence 7475, Ap
71	73	6.1	501	4	US-09-489-039A-9817	Sequence 9817, Ap
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73	72.5	6.1	746	4	US-09-205-048-4	Sequence 4, Appli
74	72.5	6.1	788	2	US-08-785-431-2	Sequence 2, Appli
75	72.5	6.1	788	4	US-09-205-048-2	Sequence 2, Appli
76	72.5	6.1	312	4	US-09-248-796A-20385	Sequence 20385, A
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83	72.5	6.1	476	3	US-08-855-213-14	Sequence 14, Appl
84	72.5	6.1	476	3	US-09-201-474-14	Sequence 14, Appl
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94	72	6.0	1038	4	US-09-585-858-11	Sequence 11, Appl
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96	72	6.0	2307	3	US-09-263-933-2	Sequence 2, Appli
97	72	6.0	2307	3	US-09-263-933-9	Sequence 9, Appli
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108	71.5	6.0	US-08-896-365-7	2	Sequence 7, Appl
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180	70	5.9	412	US-09-248-796A-22404	4	Sequence 22404, A
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183	70	5.9	471	US-09-328-314-17	3	Sequence 17, Appl
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187	69.5	5.8	321	US-09-198-452A-778	4	Sequence 778, App
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189	69.5	5.8	382	US-09-169-205D-21	4	Sequence 21, Appl
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194	69.5	5.8	557	US-09-521-195B-3	4	Sequence 3, Appli
195	69.5	5.8	557	US-09-798-743-1	4	Sequence 1, Appli
196	69.5	5.8	557	US-09-949-016-6309	4	Sequence 6309, Ap
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203	69.5	5.8	663	US-08-959-004-5	3	Sequence 5, Appli
204	69.5	5.8	676	US-09-949-016-9494	4	Sequence 9494, Ap
205	69.5	5.8	877	US-09-165-396-5	4	Sequence 5, Appli
206	69.5	5.8	1028	US-09-328-352-5749	4	Sequence 5749, Ap
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209	69.5	5.8	1704	US-08-762-500-75	3	Sequence 75, Appl
210	69.5	5.8	1704	US-09-032-438C-120	3	Sequence 120, App
211	69.5	5.8	1766	US-09-949-016-10796	4	Sequence 10796, A
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216	69	5.8	370	US-09-172-353-5	3	Sequence 5, Appli
217	69	5.8	370	US-08-776-971-21	3	Sequence 21, Appl
218	69	5.8	370	US-08-776-971-104	4	Sequence 104, App
219	69	5.8	370	US-09-799-955-5	4	Sequence 5, Appli
220	69	5.8	370	US-09-461-436B-26	4	Sequence 26, Appl
221	69	5.8	370	US-09-576-290-21	4	Sequence 21, Appl
222	69	5.8	370	US-09-576-290-104	4	Sequence 104, App
223	69	5.8	388	US-09-492-709A-378	4	Sequence 378, App
224	69	5.8	472	US-09-489-039A-8418	4	Sequence 8418, Ap
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228	69	5.8	725	US-09-248-796A-20849	4	Sequence 20849, A
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233	68.5	5.7	199	US-09-019-793A-36	4	Sequence 36, Appl
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240	68.5	5.7	383	US-08-196-989B-4	1	Sequence 4, Appli
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243	68.5	5.7	420	US-09-134-000C-5002	3	Sequence 5002, Ap
244	68.5	5.7	437	US-08-466-103A-2	2	Sequence 2, Appli
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317	3	5.7	68	US-09-368-431-36	Sequence 36, Appl
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330	503	68	5.7	1	US-08-483-094-4	Sequence 4, Appli
331	727	68	5.7	5	US-08-424-42B-2	Sequence 2, Appli
332	727	68	5.7	4	PCT-US94-05363A-2	Sequence 206, App
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343	2013	68	5.7	3	US-09-315-850-12	Sequence 12, Appl
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371	524	67.5	5.6	2	US-09-198-452A-369	Sequence 369, App
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383	153	67	5.6	4	US-09-198-452A-329	Sequence 329, App
384	159	67	5.6	3	US-09-438-185A-314	Sequence 314, App
385	159	67	5.6	4	US-09-134-000C-4969	Sequence 4969, Ap
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395	67	5.6	272	4	US-09-270-767-52945	Sequence 52945, A
396	67	5.6	282	4	US-09-270-767-35735	Sequence 35735, A
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404	67	5.6	480	3	US-08-231-368-18	Sequence 18, Appl
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406	67	5.6	496	3	US-09-046-604-18	Sequence 18, Appl
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408	67	5.6	733	4	US-09-489-039A-7885	Sequence 7885, Ap
409	67	5.6	978	4	US-09-585-858-20	Sequence 20, Appl
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457	66.5	5.6	663	3	US-09-415-582-3	Sequence 3, Appli
458	66.5	5.6	663	4	US-09-693-596-4	Sequence 4, Appli
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460	66.5	5.6	738	5	US-09-690-559-35	Sequence 35, Appl
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469	66.5	5.6	853	4	US-09-949-016-8276	Sequence 8276, Ap
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484	66.5	5.6	3010	3	US-09-014-416-3	Sequence 3, Appli
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494	66.5	5.6	3011	3	US-08-529-169A-6	Sequence 6, Appli
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565	65	5.4	182	3	US-08-925-588-8	Sequence 8, Appli
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587	65	5.4	415	4	US-09-799-978-40	Sequence 40, Appl
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589	65	5.4	415	4	US-09-710-279-780	Sequence 780, App
590	65	5.4	432	4	US-08-672-814D-2	Sequence 2, Appli
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592	65	5.4	461	2	US-09-282-218A-2	Sequence 2, Appli
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595	65	5.4	463	3	US-08-612-973-36	Sequence 36, Appl
596	65	5.4	463	3	US-08-927-597-36	Sequence 36, Appl
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598	65	5.4	490	3	US-09-949-016-11239	Sequence 11239, A
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603	65	5.4	692	3	US-09-107-532A-5138	Sequence 50, Appl
604	65	5.4	692	3	US-09-252-991A-3730	Sequence 3730, Ap
605	65	5.4	809	3	US-08-565-386-9	Sequence 9, Appli
606	65	5.4	809	4	US-09-328-352-7066	Sequence 7066, Ap
607	65	5.4	1033	4	US-09-252-991A-17395	Sequence 17395, A
608	64.5	5.4	215		US-09-107-532A-5138	Sequence 5138, Ap
609	64.5	5.4	263	1	US-09-252-991A-3730	Sequence 3730, Ap
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633	64.5	5.4	476	2	US-09-107-532A-5509	Sequence 5509, Ap
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638	64.5	5.4	487	4	US-08-855-213-20	Sequence 20, Appl
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678	64	5.4	411	3	US-09-799-978-18	Sequence 18, Appl
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692	64	5.4	504	4	US-09-710-279-920	Sequence 920, App
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763	63.5	5.3	446	4	US-09-333-696-11	Sequence 11, Appl
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768	63.5	5.3	568	3	US-09-543-681A-4949	Sequence 4949, Ap
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770	63.5	5.3	759	3	US-08-637-759B-89	Sequence 89, Appl
771	63.5	5.3	866	4	US-08-871-355A-89	Sequence 89, Appl
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827	63	5.3	1027		US-09-902-540-11750	Sequence 11750, A
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829	63	5.3	1802		US-09-586-106D-18	Sequence 18, Appl
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834	62.5	5.2	161	US-09-413-814-15	3	Sequence 15, Appl
835	62.5	5.2	183	US-09-107-532A-7197	4	Sequence 7197, Ap
836	62.5	5.2	191	US-09-270-767-40648	4	Sequence 40648, A
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840	62.5	5.2	200	US-09-270-767-51226	4	Sequence 51226, A
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858	62.5	5.2	383	PCT-US94-01321-2	5	Sequence 2, Appli
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1353	59.5	5.0	327	3	US-09-926-724-3	Sequence 3, Appli
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1355	59.5	5.0	327	4	US-09-540-236-2590	Sequence 2590, Ap
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1361	59.5	5.0	370	3	US-09-134-001C-4166	Sequence 4166, Ap
1362	59.5	5.0	388	4	US-09-222-938A-37	Sequence 37, Appl
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1368	59.5	5.0	444	4	US-09-540-236-1993	Sequence 1993, Ap
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1456	59	4.9	US-09-589-291-12	1	Sequence 12, Appl
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1482	59	4.9	US-09-575-081B-23	4	Sequence 23, Appl
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1486	59	4.9	US-08-803-973-12	1	Sequence 12, Appl
1487	59	4.9	US-08-803-972-12	1	Sequence 12, Appl

1488	59	4.9	US-08-990-114-3	2	Sequence 3, Appli
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1494	59	4.9	US-09-949-016-9676	3	Sequence 9676, Ap
1495	59	4.9	US-09-564-805-2	2	Sequence 2, Appli
1496	59	4.9	US-09-949-016-9736	4	Sequence 9736, Ap
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ALIGNMENTS

RESULT 1
US-08-691-814B-6

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;   Sequence 6, Application US/08691814B
;   Patent No. 5981218
;   GENERAL INFORMATION:
;     APPLICANT:  Rio, Marie-Christine
;     APPLICANT:  Tomasetto, Catherine
;     APPLICANT:  Basset, Paul
;     APPLICANT:  Byrne, Jennifer
;     TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful
;     TITLE OF INVENTION:  as Leukemia Markers and in Breast Cancer Prognosis
;     NUMBER OF SEQUENCES:  124
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;       STREET:  1100 New York Ave, NW, Suite 600
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0,  Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/691,814B
;       FILING DATE:  31-JUL-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/002,183
;       FILING DATE:  09-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Steffe, Eric K.
;       REGISTRATION NUMBER:  36,688
;       REFERENCE/DOCKET NUMBER:  1383.0090001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2543
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  445 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-691-814B-6
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Qy   112 ILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
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; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92

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Qy   167 ETWFLDFKV 175
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Db   326 PLLYIDYKL 334

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Qy   164 AWIETW 169
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Db   141 SWLPSY 146

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             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
             APPLICATION NUMBER: US/09/171,699
             FILING DATE: 19-Jan-1999
             CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
             APPLICATION NUMBER: US 60/015,717
             FILING DATE: 23-APR-1996
      ATTORNEY/AGENT INFORMATION:
             NAME: Kodroff, Cathy A.
             REGISTRATION NUMBER: 33,980
             REFERENCE/DOCKET NUMBER: WST66APCT
      TELECOMMUNICATION INFORMATION:
             TELEPHONE: 215-540-9200
             TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
      SEQUENCE CHARACTERISTICS:
             LENGTH: 406 amino acids
             TYPE: amino acid
             TOPOLOGY: linear
      MOLECULE TYPE: protein
      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-171-699-4

Query Match          6.7%;    Score 79.5;  DB 4;  Length 406;
Best Local Similarity 19.3%;  Pred. No. 1.8;
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Qy  121 RHWWAIALTTAVTSAFLLAK-------------VILSKLFSQGAFGYVL----+ 156
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Qy  157 ---PIISFILAWIETWFLDFKVLPQEABEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
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RESULT 6
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; Sequence 2, Application PC/TUS9402107
; GENERAL INFORMATION:
;      APPLICANT: The Wistar Institute of, Anatomy and Biology
;      TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
;      NUMBER OF SEQUENCES: 4
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Howson and Howson
;      STREET: Spring House Corporate Cntr, PO Box 457
;      CITY: Spring House
;      STATE: Pennsylvania
;      COUNTRY: USA
;      ZIP: 19477
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: PCT/US94/02107
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;      FILING DATE:
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US 08/017,130
;      FILING DATE: 12-FEB-1993
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Bak, Mary E.
;      REGISTRATION NUMBER: 31,215
;      REFERENCE/DOCKET NUMBER: WST6BPCT
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 215-540-9200
;      TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 406 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
PCT-US94-02107-2

Query Match          6.7%;    Score 79.5;  DB 5;  Length 406;
Best Local Similarity 19.3%;  Pred. No. 1.8;
Matches  52;  Conservative  36;  Mismatches  67;  Indels 115;  Gaps  12;

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Db  321 SPVPATIPLSSVIVAENSDQEESEQSDEEE 350

RESULT 7
US-09-976-594-503
; Sequence 503, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;      APPLICANT: Furness, Michael
;      APPLICANT: Buchbinder, Jenny
;      TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;      FILE REFERENCE: PA-0041 US
;      CURRENT APPLICATION NUMBER: US/09/976,594
;      CURRENT FILING DATE: 2001-10-12
;      PRIOR APPLICATION NUMBER: 60/240,409
;      PRIOR FILING DATE: 2000-10-12
;      NUMBER OF SEQ ID NOS: 1143
;      SOFTWARE: PERL Program
; SEQ ID NO 503
;      LENGTH: 723
;      TYPE: PRT
;      ORGANISM: Homo sapiens
;      FEATURE:
;      NAME/KEY: misc_feature
;      OTHER INFORMATION: Incyte ID No. 6673549 2246292CD1
US-09-976-594-503

Query Match          6.7%;    Score 79.5;  DB 4;  Length 723;
Best Local Similarity 18.0%;  Pred. No. 4;
Matches  34;  Conservative  40;  Mismatches  58;  Indels  57;  Gaps  8;
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Qy   58  FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLI----- 112
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Db   13  FMSVDICVTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

Qy   113 ---LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ----------GAFGY 154
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Db   68  VAKNSALGPRRLRASWLVISLVCLPVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124

Qy   155 VLPIISFILAWIETWFLDFKVLPQEAEEENRLL-------IVQDASERAAL--IPGGLSDGQFY----- 209
              : |||: ::|                      :::   ||| |||  |||
Db   125 ISLGASFLLWWL---------------------------LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163

Qy   210 SPPESEAGS 218
             :||| :|:
Db   164 PPPEQASGA 172
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RESULT 8
US-09-270-767-41033
; Sequence 41033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference; 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41033
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41033

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Query Match         6.6%;    Score 78.5;  DB 4;  Length 221;
Best Local Similarity    22.5%;  Pred. No. 0.97;
Matches   38;  Conservative   33;  Mismatches   73;  Indels   25;  Gaps   7;

Qy   56  CLFVTFDL---LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLI 112
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Db   17  CIYIYSSMDQPLFIILLLLLTCLSFVEXYLFVNILXIDNYIGNXNVFLFPLLLFQXII 76

Qy   113 LAYAVCRLRHWWAIALTT--AVTSAFLLAKVILSKLFSQGAFGVYL-PIISFILAWIETW 169
              :.:.:|.| |||   :.|: |:  |:||.||:  ::    |.| ::::| ::::
Db   77  VVYFCCSFCTTYQLIQGTYNSINFRFNLKNLSLT------LGFLISPPISIHFSYLPHY 129

Qy   170 FLDFKVLPQEAEEENRLL--------IVQDASERAAL--IPGGLSDGQF 208
              :: .|| :           :  ::  |||  |||
Db   130 LVNNSVLHLKNVXIQEFLDXVVKCFFILRASFRFCLKDIPNGL--GQF 176
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RESULT 9
US-09-270-767-56249
; Sequence 56249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference; 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56249
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56249

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Query Match         6.6%;    Score 78.5;  DB 4;  Length 221;
Best Local Similarity    22.5%;  Pred. No. 0.97;
Matches   38;  Conservative   33;  Mismatches   73;  Indels   25;  Gaps   7;

Qy   56  CLFVTFDL---LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLI 112
             |::  ||   :|:::  :::::  :| ::: |||:| : :| .::|: :||:|..:.||
Db   17  CIYIYSSMDQPLFIILLLLLTCLSFVEXYLFVNILXIDNYIGNXNVFLFPLLLFQXII 76

Qy   113 LAYAVCRLRHWWAIALTT--AVTSAFLLAKVILSKLFSQGAFGVYL-PIISFILAWIETW 169
              :.:.:|.| |||   :.|: |:  |:||.||:  ::    |.| ::::| ::::
Db   77  VVYFCCSFCTTYQLIQGTYNSINFRFNLKNLSLT------LGFLISPPISIHFSYLPHY 129

Qy   170 FLDFKVLPQEAEEENRLL--------IVQDASERAAL--IPGGLSDGQF 208
              :: .|| :           :  ::  |||  |||
Db   130 LVNNSVLHLKNVXIQEFLDXVVKCFFILRASFRFCLKDIPNGL--GQF 176
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RESULT 10
US-09-724-653-2
; Sequence 2, Application US/09724653
; Patent No. 6830913
; GENERAL INFORMATION:
;   APPLICANT: Ling, Victor
;   TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
;   FILE REFERENCE: APZ-004CP
;   CURRENT APPLICATION NUMBER: US/09/724,653
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: 60/167,930
;   PRIOR FILING DATE: 1999-11-29
;   NUMBER OF SEQ ID NOS: 20
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 766
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-724-653-2

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Query Match         6.6%;    Score 78.5;  DB 4;  Length 766;
Best Local Similarity    18.0%;  Pred. No. 5.7;
Matches   34;  Conservative   39;  Mismatches   59;  Indels   57;  Gaps   8;

Qy   58  FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLI----- 112
             |::|.||   ::|   :::::  :|:   |||:| :| .| ::|::||:|:|
Db   13  FMSVDICVTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

Qy   113 ---LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ----------GAFGY 154
               :.|.|:|||  .|| | : :| |:|:|::|:::
Db   68  VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124

Qy   155 VLPIISFILAWIETWFLDFKVLPQEAEEENRLL-------IVQDASERAAL--IPGGLSDGQFY----- 209
              : |||: ::|                      :::   ||| |||  |||
Db   125 ISLGASFLLWWL---------------------------LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163

Qy   210 SPPESEAGS 218
             :||| :|:
Db   164 PPPEQASGA 172
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RESULT 11
US-09-724-653-14
; Sequence 14, Application US/09724653
; Patent No. 6830913
; GENERAL INFORMATION:
;   APPLICANT: Ling, Victor
;   TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
;   FILE REFERENCE: APZ-004CP
;   CURRENT APPLICATION NUMBER: US/09/724,653
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: 60/167,930
;   PRIOR FILING DATE: 1999-11-29
;   NUMBER OF SEQ ID NOS: 20
;   SOFTWARE: PatentIn Ver. 2.0

Left column

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; SEQ ID NO 14
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-653-14

Query Match       6.6%;    Score 78.5;  DB 4;  Length 766;
Best Local Similarity  18.0%;  Pred. No. 5.7;
Matches  34;  Conservative  39;  Mismatches  59;  Indels  57;  Gaps  8;

Qy   58 FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLI----- 112
        |::|:||:| |: ||::      ::: |  :::  |:|   ::|:
Db   13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

Qy  113 ---LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ------------GAFGY 154
           |||      ||||||     ||  |: :|:
Db   68 VAKNSALGPRRLRASWLVITIVCLFVGIYAMVKLL--LFSEVRRPIRDPWFWALFVWTY 124

Qy  155 VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASRAALIPGGLSDGQFY------ 209
        :|:| |||            |: ::  || |||   :: :  : :
Db  125 ISLGASFLLWL------------------LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
        ||| :|:
Db  164 PPPEQASGA 172

RESULT 12
US-09-724-653-15
; Sequence 15, Application US/09724653
; Patent No. 6830913
; GENERAL INFORMATION:
; APPLICANT: Ling, Victor
; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: APZ-004CP
; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-653-15

Query Match       6.6%;    Score 78.5;  DB 4;  Length 766;
Best Local Similarity  18.0%;  Pred. No. 5.7;
Matches  34;  Conservative  39;  Mismatches  59;  Indels  57;  Gaps  8;

Qy   58 FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLI----- 112
        |::|:||:| |: ||::      ::: |  :::  |:|   ::|:
Db   13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

Qy  113 ---LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ------------GAFGY 154
           |||      ||||||     ||  |: :|:
Db   68 VAKNSALGPRRLRASWLVITIVCLFVGIYAMVKLL--LFSEVRRPIRDPWFWALFVWTY 124

Qy  155 VLPIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASRAALIPGGLSDGQFY------ 209
        :|:| |||            |: ::  || |||   :: :  : :
Db  125 ISLGASFLLWL------------------LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
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Db  164 PPPEQASGA 172

RESULT 13
US-09-248-796A-20444
; Sequence 20444, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
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Right column

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; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20444
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20444

Query Match       6.5%;    Score 78;  DB 4;  Length 228;
Best Local Similarity  22.1%;  Pred. No. 1.2;
Matches  32;  Conservative  32;  Mismatches  49;  Indels  32;  Gaps  7;

Qy   63 LLFVTL-----LWIIELNVN--GGIENTLEKEVMQYDYSSYF-------DIFLLAVF 106
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Db   91 LVFTALTSYGAFWLSFAAINPTFGILAAYQKDMTQLSSALAFYLIAWAILSFIFMLLTF 150

Qy  107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF----- 161
        :  |::|:   |::                |:::|::::
Db  151 KSTVLLSGFFLC-----LTALFSLLSASYFVGSVALTK--AAGAFGVIAVVAALYDTFA 202

Qy  162 ILAWIETWFLDFKVLP--QEAEEE 183
        :|   |  :|:|||    :|::
Db  203 LLATKQNSYFTLPVIPLPGSRAKQE 227

RESULT 14
US-09-270-767-43373
; Sequence 43373, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43373
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43373

Query Match       6.5%;    Score 78;  DB 4;  Length 251;
Best Local Similarity  18.8%;  Pred. No. 1.3;
Matches  34;  Conservative  46;  Mismatches  63;  Indels  38;  Gaps  6;

Qy    5 PEDMENAL--TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFD 62
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Db   51 PDSADNAVIRSGIQSNLDVQGDLN--RPTDLSSLAE------KPKDAADRPKTKGTFIDAF 103

Qy   63 LLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRH 122
        |:        :|:|                          :: |:|:
Db  104 TASISVILLTELG------------DKTFFIAAIMAMRHPRLIVFGGAIA---- 141

Qy  123 WWAIALTTAVTSAFLLAKVILSKLFSQGAFGVVLPIISFILAWIETWFLDFKVLPQEAEE 182
        ::|: |  ::||   |:::|          :::|::|:|        :|:|||
Db  142 --ALAMTILSCAFGMAANFIPKIYT----YYISTALFLIFGLKMLYDGYXMKPTDAQE 194

Qy  183 E 183
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Db  195 E 195
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RESULT 15
US-08-833-752-9
; Sequence 9, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
;   APPLICANT: SAMSON, MICHEL
;   APPLICANT: PARMENTIER, MARC
;   APPLICANT: VASSART, GILBERT
;   APPLICANT: LIBERT, FREDERICK
;   TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;   TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Knobbe, Martens, Olson & Bear
;   STREET: 620 Newport Center Drive 16th Floor
;   CITY: Newport Beach
;   STATE: CA
;   COUNTRY: U.S.A.
;   ZIP: 92660
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/833,752
;   FILING DATE: 9-APR-1997
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Altman, Daniel E
;   REGISTRATION NUMBER: 34,115
;   REFERENCE/DOCKET NUMBER: 9;
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 355 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: No. 6448375e
US-08-833-752-9

Query Match   6.5%; Score 78; DB 4; Length 355;
Best Local Similarity   23.2%; Pred. No. 2.2;
Matches   39; Conservative   25; Mismatches   60; Indels   44; Gaps   7;

Qy   62 DLLFVTLL--WI-IELNVNGGIENTLEKEVMQYDY---YSSYFDIFLLAVFRFKVLILAY 115
          |||::.|| | |::|: :| .: .: |:: : : :|||:||: : ::|
Db   80 DLLFIFTLPFWIDYKLKDDWVFGDAMCKIISGFYYTGLYSEIFFILLLTIDRYLAIVHAV 139

Qy   116 AVCRLRH---------WWAIALTTAVTSAFL--------------------LAKVIiSK 145
              | ||||| ::. : | .: |:
Db   140 FAIRARTVTFGVITSIIIWAIAIIASMPGLYFSKTQWEFTHHTCSLHFPHESLREWKLFQ 199

Qy   146 LFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEABEEN----RLLIV 189
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Db   200 ALKLNLFGLVLPLLVMIICYIGI----IKILLRRPNEKKSKAVRLIFV 243

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                    GenCore version 5.1.6

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OM protein - protein search, using sw model

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                                          (without alignments)
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

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      7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
      8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
      9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
     10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
     11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
     12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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     17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
     18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
     19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
     20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
     21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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449	1195	100.0	234	14	US-10-223-085-62	Sequence 62, Appl
466	1195	100.0	234	14	US-10-223-084-62	Sequence 62, Appl
467	1195	100.0	234	14	US-10-223-088-62	Sequence 62, Appl
468	1195	100.0	234	14	US-10-223-090-62	Sequence 62, Appl
470	1195	100.0	234	14	US-10-223-087-62	Sequence 62, Appl
478	1195	100.0	234	14	US-10-223-083-62	Sequence 62, Appl
481	1195	100.0	234	14	US-10-223-089-62	Sequence 62, Appl
498	1195	100.0	234	14	US-10-174-587-66	Sequence 66, Appl
562	1195	100.0	234	14	US-10-063-742-14	Sequence 14, Appl
640	1195	100.0	234	14	US-10-223-081-62	Sequence 62, Appl
650	1195	100.0	234	14	US-10-223-082-62	Sequence 62, Appl
665	1195	100.0	234	15	US-10-144-194A-20	Sequence 20, Appl

Result No.	Score	%	Length	N	ID	Description
670	1195	100.0	234	15	US-10-305-654-62	Sequence 62, Appl
675	1195	100.0	234	15	US-10-081-056-62	Sequence 62, Appl
681	1195	100.0	234	16	US-10-491-566-20	Sequence 20, Appl
682	1195	100.0	234	17	US-10-972-317-14	Sequence 14, Appl
683	1195	100.0	234	17	US-10-485-555-36	Sequence 36, Appl
687	1188	99.4	234	15	US-10-262-839-84	Sequence 84, Appl
688	1024	85.7	201	15	US-10-264-237-2663	Sequence 2663, Ap
689	985	82.4	198	15	US-10-262-839-82	Sequence 82, Appl
690	669.5	56.0	176	15	US-10-104-047-2567	Sequence 2567, Ap
691	664	55.6	445	14	US-10-177-293-296	Sequence 296, App
692	664	55.6	445	15	US-10-435-696-33	Sequence 33, Appl
693	625	52.3	534	18	US-10-450-763-35857	Sequence 35857, A
694	578	48.4	412	17	US-10-491-213-22	Sequence 22, Appl
695	343	28.7	580	20	US-11-097-143-6696	Sequence 6696, Ap
696	91	7.6	803	16	US-10-437-963-136814	Sequence 136814,
697	90.5	7.6	373	9	US-09-925-298-653	Sequence 653, App
698	87.5	7.3	516	14	US-10-102-806-653	Sequence 653, App
699	87	7.3	421	17	US-10-741-600-929	Sequence 929, App
700	85.5	7.2	223	17	US-10-741-600-926	Sequence 926, App
701	85.5	7.2	285	17	US-10-741-600-923	Sequence 923, App
702	85.5	7.2	315	17	US-10-741-600-924	Sequence 924, App
703	85.5	7.2	323	17	US-10-741-600-928	Sequence 928, App
704	85.5	7.2	328	17	US-10-741-600-930	Sequence 930, App
705	85	7.2	338	17	US-10-741-600-932	Sequence 932, App
706	85	7.2	339	17	US-10-741-600-927	Sequence 927, App
707	85	7.2	384	15	US-10-282-122A-54604	Sequence 54604, A
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975	72	6.0	696	16	US-10-872-972-84	Sequence 84, Appl
976	72	6.0	696	16	US-10-872-991-83	Sequence 83, Appl
977	72	6.0	696	16	US-10-872-991-84	Sequence 84, Appl
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980	72	6.0	741	14	US-10-270-878-11	Sequence 11, Appl
981	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl
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984	72	6.0	855	14	US-10-270-846-11	Sequence 11, Appl
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992	72	6.0	2307	14	US-10-191-966-9	Sequence 9, Appli
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997	71.5	6.0	363	14	US-10-262-313-8	Sequence 8, Appli
998	71.5	6.0	363	16	US-10-768-878-8	Sequence 8, Appli
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1003	71.5	6.0	382	10	US-09-904-099-1	Sequence 1, Appli
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1005	71.5	6.0	382	14	US-10-225-567A-237	Sequence 237, App
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1063	71	5.9	444	16	US-10-287-226-372	Sequence 372, App
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1494	68	5.7	714	20	US-11-097-143-41796	Sequence 41796, A
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1496	68	5.7	734	15	US-10-276-774-2313	Sequence 2313, Ap
1497	68	5.7	785	18	US-10-450-763-41049	Sequence 41049, A
1498	68	5.7	799	14	US-10-213-439-2	Sequence 2, Appli
1499	68	5.7	799	16	US-10-788-266-2	Sequence 2, Appli
1500	68	5.7	804	17	US-10-732-923-17416	Sequence 17416, A

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